

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 07:20:43 ; Search time 3213 Seconds
(without alignments)
2393.716 Million cell updates/sec

Title: US-09-758-962-1

Sequence: 1 gtcacgctatcgtacgaagct.....gaagaagagctcacatg 188

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 188 | 100.0 | 188 | 6 | AX511567 |
| 2 | 181 | 96.3 | 181 | 6 | AX511571 |
| 3 | 165 | 87.8 | 181 | 6 | AX511573 |
| 4 | 157.4 | 83.7 | 1537 | 14 | S68164 |
| 5 | 157.4 | 83.7 | 6312 | 14 | TMVPRPCP |
| 6 | 151.4 | 80.5 | 180 | 6 | AX511572 |
| 7 | 150 | 79.8 | 187 | 6 | AX511569 |
| 8 | 149 | 79.3 | 251 | 6 | AX511568 |
| 9 | 138.2 | 73.5 | 6311 | 14 | BRU03387 |
| 10 | 119 | 63.3 | 2378 | 14 | AB003936 |
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| 27 | 39 | 20.7 | 2634 | 5 | D89083 |
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| 38 | 37.8 | 20.1 | 1094 | 6 | E36785 |
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| 40 | 37.6 | 20.0 | 1490 | 6 | AR138332 |
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| 43 | 37.6 | 20.0 | 242679 | 2 | AC097122 |
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| 45 | 37.2 | 19.8 | 6037 | 12 | YSC2RAM2 |

ALIGNMENTS

RESULT 1
AX511567
LOCUS
DEFINITION
AX511567
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AX511567.1 GI:23392406

188 bp DNA linear PAT 27-SEP-2002
Santa-Cruz,S., Pogue,G.P., Toth,R.L., Chapman,S. and Carr,F.
Expression of foreign genes from plant virus vectors
Patent: WO 02055719-A 1 18-JUL-2002
BIOSOURCE GENETICS CORPORATION (US)


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REFERENCE
AUTHORS      3 (bases 1 to 6312)
              Dorokhov, Yu. L., Ivanov, P. A., Novikov, V. K., Agrianovsky, A. A.,
              Morozov, S. Yu., Efimov, V. A., Casper, R. and Atabekov, J. G.
TITLE         Complete nucleotide sequence and genome organization of a
              tobacco virus infecting cruciferae plants
JOURNAL       FEBS Lett. 350 (1), 5-8 (1994)
MEDLINE       94341372
PUBMED        7545946
REFERENCE     4 (bases 1 to 6312)
AUTHORS      Belenovich, E., Genetsov, E., Novikov, V. and Zaytsev, S.
TITLE         Properties and the genome structure of the K2 strain of tobacco
              mosaic virus
JOURNAL       Mol. Biol. (Mosk.)
REFERENCE     5 (bases 1 to 6312)
AUTHORS      Dorokhov, Y.
TITLE         Direct Submission
JOURNAL       Submitted (13-JAN-1994) Dorokhov Y., A. N. Belozersky Institute,
              Moscow State University, Moscow, Russia
REMARK        revised by author 15-MAR-94
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Query Match      83.7%; Score 157.4; DB 14; Length 6312;
Best Local Similarity 93.7%; Pred. No. 1.3e-31;
Matches 164; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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DB 5429 GTCGAAGGTTTCAAGAGTGTGTGACGAATTCGTCGATTCGGTTCGACGATTTAAACG 5488
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OY 61 GTTGCAACTTTAAAGAGAAAGAAAGAGGTGGAAGAAAGGTTAGTAAGTAAGTAT 120
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DB 5489 GTTGCAACTTTAAAGAGAAAGAAAGAGGTGGAAGAAAGGTTAGTAAGTAAGTAT 5548
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OY 121 AAGTACAGACGGGAGGAGTACGGCGGTCCTGATTCGTTATTTGAAAGAGAA 175
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DB 5549 AAGTACAGACGGGAGGAGTACGGCGGTCCTGATTCGTTATTTGAAAGAGAA 5603
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RESULT 6
LOCUS      AX511572
DEFINITION Sequence 6 from Patent WO02055719.
ACCESSION  AX511572
VERSION     AX511572.1 GI:23392411
KEYWORDS

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SOURCE
ORGANISM    Potato virus X
REFERENCE   1
  AUTHORS   Santa-Cruz, S., Pogue, G.P., Toth, R.L., Chapman, S. and Carr, F.
  TITLE     Expression of foreign genes from plant virus vectors
  JOURNAL   Patent: WO 02055719-A 6 18-JUL-2002;
            BIOSOURCE GENETICS CORPORATION (US)
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Best Local Similarity 93.4%; Pred. No. 5.1e-30;
Matches 169; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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OY 121 AAGTACAGACGGGAGGAGTACGGCGGTCCTGATTCGTTATTTGAAAGAGAGCT 180
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DB 120 AAGTACAGACGGGAGGAGTACGGCGGTCCTGATTCGTTATTTGAAAGAGAGAGCT 179
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OY 181 C 181
DB 180 C 180

RESULT 7
LOCUS      AX511569/c
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ACCESSION  AX511569
VERSION     AX511569.1 GI:23392408
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ORGANISM    Potato virus X
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            Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
REFERENCE   1
  AUTHORS   Santa-Cruz, S., Pogue, G.P., Toth, R.L., Chapman, S. and Carr, F.
  TITLE     Expression of foreign genes from plant virus vectors
  JOURNAL   Patent: WO 02055719-A 3 18-JUL-2002;
            BIOSOURCE GENETICS CORPORATION (US)
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Best Local Similarity 96.8%; Pred. No. 1.2e-29;
Matches 153; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 180 AATCGTCGATTCGGTTCACGATTTAAAGGCTGACAACTTTAAAGAGAGAAAGA 121
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OY 89 AGGTTGAAGAAAGGAGTGTAGTAAGTAAGTAAAGTACAGACCGAGAGTACCGCGGTC 148
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DB 120 AGGTTGAAGAAAGGAGTGTAGTAAGTAAGTAAAGTACAGACCGAGAGTACCGCGGTC 61
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OY 149 CTGATTCGTTATTTGAAAGAGAGAGAGCTCACCAT 186

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Db      60 CTGATTCGTTTAATTGAAGAGAAAGATTGCATAT 23
RESULT 8
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LOCUS   AX511568
DEFINITION Sequence 2 from Patent WO02055719.
ACCESSION AX511568
VERSION  AX511568.1 GI:23392407
KEYWORDS
SOURCE  Potato virus X
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
REFERENCE 1
AUTHORS Santa-Cruz,S., Pogue,G.P., Toth,R.L., Chapman,S. and Carr,F.
TITLE    Expression of foreign genes from plant virus vectors
JOURNML  Patent: WO 02055719-A 2 18-JUL-2002;
BIOSOURCE GENETICS CORPORATION (US)
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Query Match 79.3%; Score 149; DB 6; Length 251;
Best Local Similarity 100.0%; Pred. NO. 2.2e-29;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 97 CGAATTCGTCGATTCGTTGAGCATTAAAGCGGTTGACAACTTTAAAGAGAAAA 156
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OY 87 GAAGGTGAGAGAGAGGCTAGTAGTACGTATAGTACAGAGCCGAGAGTACGCCGG 146
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Db 157 GAAGGTGAGAGAGAGGCTAGTAGTACGTATAGTACAGAGCCGAGAGTACGCCGG 216
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OY 147 TCCGATTCGTTTAATTGAAGAGAAAA 175
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Db 217 TCCGATTCGTTTAATTGAAGAGAAAA 245
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RESULT 9
BRU03387
LOCUS   BRU03387
DEFINITION Turnip vein-clearing virus, complete genome.
ACCESSION U03387.1 GI:2894629
VERSION  U03387.1 GI:2894629
KEYWORDS
SOURCE  Turnip vein-clearing virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
REFERENCE 1
AUTHORS Larterey,R.T., Voss,T.C. and Melcher,U.K.
TITLE    Electron microscopic and molecular characterization of turnip
    vein-clearing virus
JOURNML Arch. Virol. 138 (3-4), 287-298 (1994)
MEDLINE 95091521
PUBMED  7998835
REFERENCE 2 (bases 1 to 67; 3392 to 6311)
AUTHORS Larterey,R.T., Voss,T.C. and Melcher,U.K.
TITLE    Completion of a cDNA sequence from a tobamovirus pathogenic to
    crucifers
JOURNML Gene 166, 321-322 (1995)
REFERENCE 3 (bases 1 to 6311)
AUTHORS Melcher,U.K.
TITLE    Direct Submission
JOURNML Submitted (09-NOV-1993) Biochemistry & Molecular Biology, Oklahoma
    State University, NRC 246, Stillwater, OK 74078-0454, USA
REFERENCE 4 (bases 1 to 6311)
AUTHORS Melcher,U.K.

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TITLE    Direct Submission
JOURNAL  Submitted (18-FEB-1998) Biochemistry & Molecular Biology, Oklahoma
    State University, NRC 246, Stillwater, OK 74078-0454, USA
REMARK   Sequence update by submitter
COMMENT   On Feb 18, 1998 this sequence version replaced gi:619581.
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        KNVCTCFAEFHEHMLDCTVLDLGATFQKSGDNLSEFFHNESTLTHSNI
        IRYVCKTFEPASQRFVHKEFLVNVNMYCKFTFVDVFTLFRGYHNNVOCSEERYA
        MDAWHYKRTLAMNAERTIFPDNALNPEFVKYADVIYVLPDASITTGMSREIM
        VNKDEVYVNHKITVYQAKALYANVLSFVSIISRVINVTARSEMDTKAIIIGPL
        AMTEFLIRKIGHVODEITLKKRQKEDRTNTEILSCDALMGVIRPSKTELYNGFY
        KYABALRIKPELCTTRADRLVLOYKAAEEROSDLSKPLESEKRTNALSLSVLE
        NIDSDLEAFETLCOQKNDVPMKAVVLAHKSLLTLPKRPEEELISELKRQEGS
        CAHEKEVLSQNDAPFCVKNLVESGVAYGACPGGGFDRDLVDIDFHLKSDAVK
        KGTWMSAVYTSIKVQOKNVIYDLSASLAVSNLCAVLRDVGVDSEQSGVMD
        VRRGFWMLKPNKSHAMGVAEDANHKIYVILNMDGKPCVDETFRVAVSDELITS
        DMGRTKTLTSCSPNGEPPEPNKAVILNDVGCGGCTKREITIKVESDILLVPEKAS
        KMIIRANQAVYIRADKRNRYVDSFLMHSRPFKRLFTDEGLMLHFGCNFLLLS
        QCDVAVYIGDKQIPEICRVAFPYPAHFALVADKERVNRTILRCPEADVIYFLNKY
        DGAVNTGSVAERVAEYVGRGALNPITLLEGLILFTQADKFLKEDVYFVFNKY
        HEVQGETEKAIVALTSTPLEIISASPHVNLVARTTCCKTYVVLADYVALLISE
        MEKLSNFFLDNRYVAGVOYOLIDAVRDSNLVLPQRPKSGMDMVOYDVALVGNIS
        TILNEPDVATNINDISLNVKDCRIDESQVLPREGQIFLRKRTAAEPPRRAGIL
        ENLYAMIKRNARADPLGTITIEDTASLVKRFNDYVDSKESGNETMTRESFRR
        LSKOESSVQGLADPNEVDLPVADVEYKIMNISQPKLIDLSIODEYPALQIYVHSK
        INALTFGPFSLETRMLERIDSKEFLFTRTPAQIDIEFSDLDSTQAMETILEDISK
        YDKSONEPRCAVEYKIMERLGIIDELIACVMOGHRKTLTKDYTAGVTKCLMYORSGD
        VTTFPGNTIITIAACSSMIPMDKVIYKAFGDDSLIYIPKGLDLPDIOAGALMNPFE
        AKLFRKRYGRCGRVYIHHDRGAIYVYDPLTISKLGKTHIRDYVHLEELRESLCDVA
        SNLNCATFSOLDENAVAEHKTAVGGSFAFSIITIKYLSDKRLFDFLFPV"

```


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OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 05:23:28 ; Search time 281 Seconds

(without alignments)
1806.030 Million cell updates/sec

Title: US-09-758-962-1

Perfect score: 188

Sequence: 1 gtcgcgcgtatcgcataaact.....gaagaagaagctcaccatg 188

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : N_Geneseq.19Jun03.*

| | |
|-----|--|
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| 2: | /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.* |
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| 22: | /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.* |
| 23: | /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.* |
| 24: | /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.* |
| 25: | /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1 | 188 | 100.0 | 188 | 24 | ABQ76058 | Clone TXS.GFP-IRRS |
| 2 | 181 | 96.3 | 181 | 24 | ABQ76062 | Clone TXS.GFP-IRRS |
| 3 | 165 | 87.8 | 181 | 24 | ABQ76064 | Clone SC197 contai |
| 4 | 151.4 | 80.5 | 180 | 24 | ABQ76063 | Clone SC196 conta |
| 5 | 150 | 79.8 | 187 | 24 | ABQ76060 | Clone TXS.GFP-SERT |
| 6 | 149 | 79.3 | 251 | 24 | ABQ76059 | Clone TXS.GFP-HIRE |
| 7 | 148 | 78.7 | 148 | 25 | ABZ57802 | Crucifer tobacco v |
| 8 | 148 | 78.7 | 148 | 25 | ABV5164 | Crucifer tobacco m |

| | | | | | | |
|----|------|------|-------|----|----------|--------------------|
| 9 | 148 | 78.7 | 152 | 24 | NA149136 | IRRS element IRRSC |
| 10 | 88.8 | 47.2 | 1543 | 20 | AA87568 | Ribgrass mosaic vi |
| 11 | 43.4 | 23.1 | 6215 | 24 | AA310982 | PBSRT27 vector con |
| 12 | 43.4 | 23.1 | 7252 | 24 | AA310982 | Plasid transforma |
| 13 | 43.4 | 23.1 | 7252 | 24 | AA310982 | PHK05 vector conta |
| 14 | 43.4 | 23.1 | 13917 | 24 | AA31037 | Plasid transforma |
| 15 | 41.8 | 22.2 | 1456 | 21 | AA359645 | Human secreted pro |
| 16 | 41.2 | 21.9 | 1566 | 25 | AA359645 | Human secreted pro |
| 17 | 40.2 | 21.4 | 526 | 25 | AB61084 | Arabidopsis thalia |
| 18 | 39.8 | 21.2 | 418 | 25 | AB61084 | Arabidopsis thalia |
| 19 | 39.4 | 21.0 | 5491 | 25 | AA546390 | Tumour suppressor |
| 20 | 39.2 | 20.9 | 327 | 25 | AB60706 | Arabidopsis thalia |
| 21 | 39 | 20.7 | 759 | 19 | AAV01704 | Hormone-like prote |
| 22 | 38.8 | 20.6 | 1353 | 24 | ABK52453 | Accessary factor T |
| 23 | 38.8 | 20.6 | 4102 | 19 | AAV4257 | Plasid PRK9/10 DN |
| 24 | 38.6 | 20.5 | 2128 | 22 | AAV45092 | Human secreted pro |
| 25 | 38.4 | 20.4 | 382 | 25 | AB61374 | Human secreted pro |
| 26 | 38 | 20.2 | 361 | 21 | AA359649 | Human secreted pro |
| 27 | 38 | 20.2 | 434 | 25 | AB61310 | Arabidopsis thalia |
| 28 | 38 | 20.2 | 465 | 25 | AB61384 | Arabidopsis thalia |
| 29 | 38 | 20.2 | 616 | 20 | AA32262 | Human secreted pro |
| 30 | 37.8 | 20.1 | 122 | 24 | ABQ76061 | Clone TXS.GFP-IRRS |
| 31 | 37.8 | 20.1 | 259 | 16 | AAQ87664 | Mouse azoospermia |
| 32 | 37.8 | 20.1 | 334 | 23 | ABV49911 | Human prostate exp |
| 33 | 37.8 | 20.1 | 391 | 23 | ABV38458 | Human prostate exp |
| 34 | 37.8 | 20.1 | 587 | 20 | AA37393 | Human secreted pro |
| 35 | 37.6 | 20.1 | 1094 | 20 | AA329498 | S. aureus MuRF ORF |
| 36 | 37.6 | 20.0 | 516 | 21 | AA427947 | Terminal sequence |
| 37 | 37.6 | 20.0 | 1490 | 16 | AAQ75361 | Gibberellin-20-ox |
| 38 | 37.6 | 20.0 | 4941 | 25 | AA353366 | Transformation vec |
| 39 | 37.4 | 19.9 | 472 | 23 | ABV38497 | Human prostate exp |
| 40 | 37.4 | 19.9 | 1828 | 22 | AAV32757 | Human secreted pro |
| 41 | 37.2 | 19.8 | 478 | 23 | ABV36096 | Human prostate exp |
| 42 | 37.2 | 19.8 | 478 | 23 | ABV45153 | Human prostate exp |
| 43 | 36.8 | 19.6 | 146 | 21 | AA359712 | Human secreted pro |
| 44 | 36.8 | 19.6 | 4898 | 21 | AA359712 | Preliminary CIASP- |
| 45 | 36.8 | 19.6 | 4898 | 21 | AA359712 | Preliminary CIASP- |

ALIGNMENTS

RESULT 1
ABQ76058
ABQ76058 strand: DNA; 188 BP.

AC ABQ76058;
XX
XX 30-SEP-2002 (first entry)
XX
XX Clone TXS.GFP-IRRS-CP containing IRRS DNA sequence.
XX
XX
XX IRRS; Internal ribosome entry site; viral protein; bicistronic;
XX virus infection; coat protein; protein replacement therapy; crop;
XX nutritional value; seed oil content; ds.
XX
XX Synthetic.
XX
XX WO200255719-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-US01123.
XX
XX 09-JAN-2001; 2001US-0758962.
XX
XX (BIOS-) BIOSOURCE GENETICS CORP.
XX Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F;
XX WPI: 2002-557829/59.
XX
XX New polypeptides contained in plant virus expression vectors, as gene

PT expression tools, in protein replacement therapy or for intervening in
PT a metabolic pathway to improve the nutritional value of a crop or alter
PT the oil content of seeds -

Claim 4; Fig 3; 33pp; English.

This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open reading frame (ORF) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a recombinant poliovirus X-based viral vector containing a nucleic acid construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosome entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TXS.GFP.IRESs-CP containing an IRES region described in the method of the invention.

S0 Sequence 188 BP; 66 A; 26 C; 51 G; 45 T; 0 other;

| | | | | |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match | 100.0% | Score 188; | DB 24; | Length 188; |
| Best Local Similarity | 100.0%; | Pred. No. 7.7e-44; | | |
| Matches 188; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0 |

| | | | |
|-----|-----|---|-----|
| Oy | I | GTCGACGGTATCGATTAAGCTTGATTCGAATCCGTCAATTCGGTTGCAGATTAAAGCG | 60 |
| Oy | I | GTCGACGGTATCGATTAAGCTTGATTCGAATCCGTCAATTCGGTTGCAGATTAAAGCG | 60 |
| Ddb | 1 | GTCGACGGTATCGATTAAGCTTGATTCGAATCCGTCAATTCGGTTGCAGATTAAAGCG | 60 |
| Oy | 61 | GTTGACAACCTTTAAAAGAAGAAAAAGAAGGTTGAGAAAAAGGCTGTAGTAGTAAGTAT | 120 |
| Ddb | 61 | GTTGACAACCTTTAAAAGAAGAAAAAGAAGGTTGAGAAAAAGGCTGTAGTAGTAAGTAT | 120 |
| Oy | 121 | AAGTACAGACCAGGAGAAAGTACGCCGGTCCGTGATTCGTTAATTGAAAGAAAGAGCT | 180 |
| Oy | 121 | AAGTACAGACCAGGAGAAAGTACGCCGGTCCGTGATTCGTTAATTGAAAGAAAGAGCT | 180 |
| Ddb | 121 | AAGTACAGACCAGGAGAAAGTACGCCGGTCCGTGATTCGTTAATTGAAAGAAAGAGCT | 180 |
| Oy | 181 | CACCATGG | 188 |
| Oy | 181 | | |
| Ddb | 181 | CACCATGG | 188 |

```

RESULT 2
ABQ76062
ID      ABQ76062 standard; DNA; 181 BP

```

DT 30-SEP-2002 (first entry)

Clone TXS.GFP-IRES-CP containing IREScp DNA sequence

KM IRES; internal ribosome entry site; viral protein; bicistronic;
KM virus infection; coat protein; protein replacement therapy; crop
KM nutritional value; seed oil content; ds.

Synthetic

PN .W0200255719-A2

18-JUL-2002

09-JAN-2002; 2002WO-US01123

09-JAN-2001; 2001US-0758962

PA (BIOS-) BIOSOURCE GENETICS CORP.

PI Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F, ...

DR WPI; 2002-557829/59.

PT New polypeptides contained in plant virus expression vectors, as gene
PT expression tools, in protein replacement therapy or for intervening in
PT a metabolic pathway to improve the nutritional value of a crop or alter
PT the oil content of seeds -

Claim 4; Fig 4; 33pp; English.

This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open reading frame (ORF) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a recombinant potex virus X-based viral vector containing a nucleic acid construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosome entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone TXS.GFP.IRES5-CP containing an IRES3P region described in the method of the invention.

50 Sequence 181 BP; 64 A; 24 C; 49 G; 44 T; 0 other

| | | | | |
|---------------------------|--------|--------------------|--------|------------------|
| Query Match | 96.3% | Score 181; | DB 24; | Length 181; |
| Best Local Similarity | 100.0% | Pred. No. 7.3e-42; | | |
| Matches 181; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0 |

| | | | |
|----|-----|--|--|
| QY | 1 | GTGCAAGCGTATGATGAATACCTTGATTCGCAATTCGCGATTCGGTGGAGCAATTTAAAGCG | 60 |
| | | 1 | GTGCAAGCGTATGATGAATACCTTGATTCGCAATTCGCGATTCGGTGGAGCAATTTAAAGCG |
| Db | 1 | GTGCAAGCGTATGATGAATACCTTGATTCGCAATTCGCGATTCGGTGGAGCAATTTAAAGCG | 60 |
| QY | 61 | GTTCACAACCTTTAAAGAAGGAAAAAGAGTTGACAAAAAGGCTGTAGTAAGTAACTAT | 120 |
| | | 61 | GTTCACAACCTTTAAAGAAGGAAAAAGAGTTGACAAAAAGGCTGTAGTAAGTAACTAT |
| Db | 61 | GTTCACAACCTTTAAAGAAGGAAAAAGAGTTGACAAAAAGGCTGTAGTAAGTAACTAT | 120 |
| QY | 121 | AAGTACAGACCGGAGAGTACGCCGGCTCTGATTCGTTAAATTTGAAGAAGAAAGAGCT | 180 |
| | | 121 | AAGTACAGACCGGAGAGTACGCCGGCTCTGATTCGTTAAATTTGAAGAAGAAAGAGCT |
| Db | 121 | AAGTACAGACCGGAGAGTACGCCGGCTCTGATTCGTTAAATTTGAAGAAGAAAGAGCT | 180 |
| QY | 181 | C | 181 |
| | | 181 | C |
| Db | 181 | C | 181 |

RESULT 3
ABQ76064
ID ABQ76064 standard; DNA; 181 BP

AC ABQ76064;

DT 30-SEP-2002 (first entry)

DE Clone SC197 containing IRES_{sc} DNA sequence.
XX
XX
XX IRES; internal ribosome entry site; viral protein; bicistronic;
XX

KW **nutritional**

OS Synthetic.

Claim 4; Flg 4; 33pp; English.

Sequence 181 BP; 61 A; 28 C; 53 G; 39 T; 0 other;

1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGTTGCAGCATTAAAGCG 60

b 1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTCGGCTGCAGCATTAAAGCG 60

181 C 181

181 C 181

ABQ76063

30-SEP-2002 (first entry)

Clone SC196 containing IREScp DNA sequence.

OS Synthetic

PN : W0200255719-A2

PD 18-JUL-2002

PF 09-JAN-2002; 2002WO-US01123.

PR 09-JAN-2001; 2001US-0758962.

PA (BIOS-) BIOSOURCE GENETICS CORP.

PI Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F, ...

DR WPI; 2002-557829/59.

PS Claim 4; Fig 4; 33pp; English.

This invention describes a novel isolated polynucleotide comprising an internal ribosome entry site (IRES) nucleotide sequence, an open reading frame (ORF1) encoding a peptide and an ORF2 encoding a viral protein, where the IRES is located between ORF1 and ORF2. The novel polynucleotides of the invention are used in the construction of a recombinant potato virus X-based viral vector containing a nucleic acid construct comprising a bicistronic message with an intervening IRES. The constructs are used in a method for regulating the rate at which a virus infection spreads in a host. Regulation is achieved by placing the nucleic acid construct comprising an internal ribosomes entry site upstream of a coat protein gene, where the IRES is chosen by the rate of infection of the viral vector on a host in the presence of that IRES. The polynucleotide and vectors of the invention are useful for directing rapid and high-level expression of foreign genes in mature, differentiated, plant tissue. These are particularly useful in protein replacement therapy, or for intervening in a metabolic pathway to improve the nutritional value of a crop or alter the oil content of the seed. This sequence represents a fragment of the clone SC196 containing an IRESop region described in the method of the invention.

Sequence 180 BP; 60 A; 31 C; 52 G; 37 T; 0 other;

| | | | | |
|-----------------------|----------------|-------------------|----------|------------|
| Query Match | 80.5% | Score 151.4 | DB 2 | Length 180 |
| Best Local Similarity | 93.4% | Pred. No. 1.8e-33 | | |
| Matches 169 | Conservative 0 | Mismatches 11 | Indels 1 | Gaps 1 |

9Y 1 GTCGACGGTATCGATAAGCTTGATATCGAATTCGTCGATTGGTTGCAGCATTAAAGCG 60

Db 1 GTCGACGGTATCGATAAGCCTGATATCGAACTCGCCGATTGGGGTCTGCA-TTAAAGCG 59

61 GTGACAACTTTAAAGAAGGAAAGAAGGTTGAAGAAAGGCTAGTAAGTAT 120

Db 60 GCTGACAACTTAAAGAGGAAAGAGGGTTGAAGAAAGGGTGTAGTAAGTAT 119

121 AAGTACAGACCGAGAGTACGCCGGTCTGATTGTTAATTGAAAGAGAAGAGCT 180

Db 120 AAGTACAGACCGCGAAGTGGCGCGGTCTGATTCGTTTAATTGAAAGAGAAGAGCT 179

QY 181 C 181

Db 180 C 180

RESULT 5
ABQ76060/c
ID ABQ76060 standard; DNA; 137 BP

```

XX ABQ76060;
AC 30-SEP-2002 (first entry)
XX
XX Clone TKS.GFP-SERI-CP containing IRES DNA sequence.
XX
XX IRES: Internal ribosome entry site; viral protein; bicistronic;
XX virus infection; coat protein; protein replacement therapy; crop;
XX nutritional value; seed oil content; ds.
XX
XX Synthetic.
XX
XX MO200255719-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-US01123.
XX
XX 09-JAN-2001; 2001US-0758962.
XX
XX (BIOS-) BIOSOURCE GENETICS CORP.
XX
XX Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F;
XX MPI; 2002-557829/59.
XX
XX New polypeptides contained in plant virus expression vectors, as gene
XX expression tools, in protein replacement therapy or for intervening in
XX a metabolic pathway to improve the nutritional value of a crop or alter
XX the oil content of seeds.
XX
XX Claim 4; Fig 3; 33pp; English.
XX
XX This invention describes a novel isolated polynucleotide comprising an
XX internal ribosome entry site (IRES) nucleotide sequence, an open reading
XX frame (ORF) encoding a peptide and an ORF2 encoding a viral protein,
XX where the IRES is located between ORF1 and ORF2. The novel
XX polynucleotides of the invention are used in the construction of a
XX recombinant potato virus X-based viral vector containing a nucleic acid
XX construct comprising a bicistronic message with an intervening IRES. The
XX constructs are used in a method for regulating the rate at which a virus
XX infection spreads in a host. Regulation is achieved by placing the
XX nucleic acid construct comprising an internal ribosome entry site
XX upstream of a coat protein gene, where the IRES is chosen by the rate of
XX infection of the viral vector on a host in the presence of that IRES. The
XX polynucleotide and vectors of the invention are useful for directing
XX rapid and high-level expression of foreign genes in mature,
XX differentiated, plant tissue. These are particularly useful in protein
XX replacement therapy, or for intervening in a metabolic pathway to improve
XX the nutritional value of a crop or alter the oil content of the seed.
XX This sequence represents a fragment of the clone TKS.GFP-SERI-CP
XX containing an IRES region described in the method of the invention.
XX
XX Sequence 187 BP; 45 A; 47 C; 27 G; 68 T; 0 other;
XX
XX Query Match 79.8%; Score 150; DB 24; Length 187;
XX Best Local Similarity 96.8%; Pred. No. 4.4e-33;
XX Matches 153; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

RESULT 6
ABQ76059
ID ABQ76059 standard; DNA; 251 BP.
XX
XX ABQ76059;
XX
XX 30-SEP-2002 (first entry)
XX
XX Clone TKS.GFP-HIRS-CP containing IRES DNA sequence.
XX
XX IRES: Internal ribosome entry site; viral protein; bicistronic;
XX virus infection; coat protein; protein replacement therapy; crop;
XX nutritional value; seed oil content; ds.
XX
XX Synthetic.
XX
XX MO200255719-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-US01123.
XX
XX 09-JAN-2001; 2001US-0758962.
XX
XX (BIOS-) BIOSOURCE GENETICS CORP.
XX
XX Santa-Cruz S, Pogue GP, Toth RL, Chapman S, Carr F;
XX MPI; 2002-557829/59.
XX
XX New polypeptides contained in plant virus expression vectors, as gene
XX expression tools, in protein replacement therapy or for intervening in
XX a metabolic pathway to improve the nutritional value of a crop or alter
XX the oil content of seeds.
XX
XX Claim 4; Fig 3; 33pp; English.
XX
XX This invention describes a novel isolated polynucleotide comprising an
XX internal ribosome entry site (IRES) nucleotide sequence, an open reading
XX frame (ORF) encoding a peptide and an ORF2 encoding a viral protein,
XX where the IRES is located between ORF1 and ORF2. The novel
XX polynucleotides of the invention are used in the construction of a
XX recombinant potato virus X-based viral vector containing a nucleic acid
XX construct comprising a bicistronic message with an intervening IRES. The
XX constructs are used in a method for regulating the rate at which a virus
XX infection spreads in a host. Regulation is achieved by placing the
XX nucleic acid construct comprising an internal ribosome entry site
XX upstream of a coat protein gene, where the IRES is chosen by the rate of
XX infection of the viral vector on a host in the presence of that IRES. The
XX polynucleotide and vectors of the invention are useful for directing
XX rapid and high-level expression of foreign genes in mature,
XX differentiated, plant tissue. These are particularly useful in protein
XX replacement therapy, or for intervening in a metabolic pathway to improve
XX the nutritional value of a crop or alter the oil content of the seed.
XX This sequence represents a fragment of the clone TKS.GFP-HIRS-CP
XX containing an IRES region described in the method of the invention.
XX
XX Sequence 251 BP; 72 A; 51 C; 76 G; 52 T; 0 other;
XX
XX Query Match 79.3%; Score 149; DB 24; Length 251;
XX Best Local Similarity 100.0%; Pred. No. 9.1e-33;
XX Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

| | | | |
|-----------------------|---|--|-----|
| OY | 148 | CCGATTGGTTTAATTTGAAGAAGAAA | 175 |
| Dd | 121 | CCTGATTCGTTTAAATTTGAAGAAGAAA | 148 |
| | | | |
| RESULT 8 | | | |
| ID | ABV75164 | ABV75164 standard; DNA; 148 BP. | |
| AC | ABV75164; | | |
| DT | 19-FEB-2003 | (first entry) | |
| DE | Crucifer tobacco mosaic virus IRES element IREScpl48cr. | | |
| XX | Transcription; plant; Internal ribosome entry site; IRES; transgenic; ds. | | |
| OS | Tobacco mosaic virus. | | |
| PN | WO200283867-A2. | | |
| PD | 24-OCT-2002. | | |
| PF | 17-APR-2002; 2002MO-USI1924. | | |
| PR | 17-APR-2001; 2001US-284239P. | | |
| PA | (ICON-) ICON GENETICS INC. | | |
| PI | Gleba Y, Bascomb N, Bossie M, Hall G, Petty TJ; | | |
| DR | WPI; 2003-067578/06. | | |
| XX | | | |
| PT | Identifying and characterizing transcriptionally active regions in | | |
| PT | plants, useful for producing transgenic plants, comprises inserting | | |
| PT | nucleic acid constructs (called landing pads) with internal ribosome | | |
| PT | entry sites(s) into plant genes | | |
| PS | | | |
| XX | Disclosure; Page 17; 50pp; English. | | |
| CC | The invention relates to identifying and characterizing transcriptionally | | |
| CC | active regions in plants. The method involves (a) inserting into the | | |
| CC | plant a genomic nucleic acid construct comprising at least one internal | | |
| CC | ribosome entry site (IRES) in operable association with a reporter gene; | | |
| CC | and (b) detecting the expression of the reporter gene as an indication of | | |
| CC | insertion of the nucleic acid construct into a transcriptionally active | | |
| CC | region. The method for identifying and characterizing transcriptionally | | |
| CC | active regions in plants, is useful for producing transgenic plants and | | |
| CC | seeds, as is the method for introducing a nucleic acid into plants. The | | |
| CC | method is also useful for observing or measuring phenotype in an | | |
| CC | organism. The present sequence represents an IRES element derived from | | |
| CC | the genome of the crucifer tobacco mosaic virus (CRTMV). | | |
| SO | | | |
| Sequence | 148 BP; 56 A; 17 C; 40 G; 35 T; 0 other; | | |
| | | | |
| Query Match | 78.7%; Score 148; DB 25; Length 148; | | |
| Best Local Similarity | 100.0%; Pred. No. 1.5e-32; | | |
| Matches 148: | Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| OY | 28 | GAATTCGTGCATTCGGTTGCAGCAATTTAAGCGGTTGACAATTAAAGAAGANAAG 87 | |
| Dd | 1 | GAATTCGTGCATTCGGTTGCAGCAATTTAAGCGGTTGACAATTTAAAGAAGANAAG 60 | |
| OY | 88 | AAGTTAAGAAAAAGGCTGTAGTAGTAAGTAGTAAGTAGCAGACCGAGAGTAAGCCCGT 147 | |
| Dd | 61 | AAGTTAAGAAAAAGGCTGTAGTAGTAAGTAGTAAGTAGCAGACCGAGAGTAAGCCCGT 120 | |
| OY | 148 | CCTGATTCGTTTAAATTTGAAGAAGAAA 175 | |
| Dd | 121 | CCTGATTCGTTTAAATTTGAAGAAGAAA 148 | |
| | | | |
| RESULT 9 | | | |

| ID | AAI49136 | AAI49136 standard; RNA: 152 BP. |
|----|---|--|
| XX | AAI49136; | |
| AC | 07-NOV-2002 (first entry) | |
| DT | IRES element IRESCP148Crdar. | |
| XX | Plant vector system; transfection; tobomavirus vector; plant; transgenic; | |
| DE | protein production; ss. | |
| KW | Unidentified. | |
| XX | | |
| OS | | |
| XX | | |
| PH | Key | Location/Qualifiers |
| FT | misc_binding | 88..94 |
| FT | | /*tag- a |
| FT | stem_loop | /bound_motety- "binds nucleotides 135-129 of itself" |
| FT | | 95..101 |
| FT | stem_loop | /*tag- b |
| FT | | 102..127 |
| FT | | /*tag- c |
| FT | misc_binding | 129..135 |
| FT | | /*tag- d |
| FT | | /bound_motety- "binds nucleotides 94-88 of itself" |
| PN | DEI0109354-A1. | |
| PD | 05-SEP-2002. | |
| XX | | |
| XX | 27-FEB-2001; 2001DE-1009354. | |
| XX | | |
| PR | 27-FEB-2001; 2001DE-1009354. | |
| XX | | |
| PA | (ICON-) ICON GENETICS AG. | |
| PI | Klimyuk V, Benning G, Gleba Y; | |
| DR | WPI; 2002-620293/67. | |
| XX | | |
| PT | Controlling biochemical processes in plants, useful for producing e.g. | |
| PT | pharmaceutical peptides, from interaction between components in genome | |
| XX | and viral transfer vector | |
| PS | Disclosure; Fig 20; 92pp; German. | |
| XX | | |
| CC | The present invention relates to a method of controlling a selected | |
| CC | biochemical process or cascade in a plant. This involves the introduction | |
| CC | of a heterologous DNA sequence into the plant genome, and infection by a | |
| CC | viral transfer vector containing a second heterologous sequence, which is | |
| CC | able to cause the first sequence to be switched on. The method is used to | |
| CC | produce selected gene products in transgenic plants, particularly | |
| CC | pharmaceutical polypeptides but also sugars and biodegradable polymers. | |
| CC | The present sequence is an RNA sequence described in the exemplification | |
| CC | of the invention. | |
| XX | | |
| XX | | |
| XX | Sequence 152 BP; 57 A; 17 C; 41 G; 37 U; 0 other; | |
| QW | | |
| QW | Query Match | 78.7%; Score 148; DB 24; Length 152; |
| QW | Best Local Similarity | 76.4%; Pred. No. 1.6e-32; |
| QW | Matches 113; Conservative 35; Mismatches 0; Indels 0; Gaps 0 | |
| DB | 1 GAATTCGTCGATTCGTTGCAGCATTTAAACGGGTGACACTTAAAGAGAAGAAG 87 | |
| QY | : : : : : : : : : : | |
| DB | 1 AAGTTCGTCGATTCGTTGCAGCATTTAAACGGGTGACACTTAAAGAGAAGAAG 60 | |
| QY | 88 AAGTTGAAGAAAGGGTGTAGTAAGTAAGTAAGTACAGACCGGAGAGTACGCCGT 147 | |
| QY | : : : : : : : : : | |
| DB | 61 AAGGUTGAAGAAAGGGGUGUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUGAUG 120 | |
| QY | 148 CCTGATTCGTTTAATTGAAGAGAA 175 | |
| QY | : : : : : : : : : | |
| DB | 121 CCGAATTCGTTTAATTGAAGAGAA 148 | |

| |
|--|
| RESULT 10 |
| AAx87568 |
| ID AAx87568 standard; cDNA; 1543 BP. |
| XX. |
| AC AAx87568; |
| DT |
| XX |
| 08-OCT-1999 (first entry) |
| DE Ribgrass mosaic virus cDNA fragment. |
| XX |
| Gene function: protein function: tobamovirus; coat protein; vector; |
| KM ss. |
| XX |
| Ribgrass mosaic virus. |
| OS |
| PN MO936516-A2. |
| XX |
| PD 22-JUL-1999. |
| XX |
| Pf 15-JAN-1999; 99MO-US01164. |
| XX |
| PR 16-JAN-1998; 98US--0008186. |
| XX |
| (BIOS-) BIOSOURCE TECHNOLOGIES INC. |
| PA |
| XX |
| Pi Della-Cioppa G, Erwin RL, Fitzmaurice WP, Hanley KM: |
| PI Kunagel MH, Lindbo JA, McGee DR, Padgett HS, Pogue GP; |
| DR WPI: 1999-458459/38. |
| XX |
| Determining the function of polynucleotide sequences and their |
| PT encoded proteins by transfecting them into a host organism |
| PS Example 12: Page 65-66; 156pp; English. |
| XX |
| This is the nucleotide sequence of a ribgrass mosaic virus cDNA |
| CC fragment in vector plasmid KS+. The sequence includes the 30K |
| CC subgenomic promoter, coat protein open reading frame and 3' end. |
| CC It was obtained by PCR amplification. The cDNA was used in the |
| CC construction of a tobamoviral vector for expression of heterologous |
| CC genes in Arabidopsis thaliana. The invention provides methods for |
| CC rapidly determining the function of nucleic acid sequences by |
| CC transfecting them into a host organism to effect expression, and |
| CC analysing the resulting phenotypic and biochemical changes. |
| CC Methods for silencing endogenous genes, for selecting desired |
| CC functions of RNAs and proteins, and for inhibiting an endogenous |
| CC protease in a plant host are also provided. |
| XX |
| SQ Sequence 1543 BP; 433 A; 280 C; 396 G; 434 T; 0 other; |
| Query Match 47.2%; Score 88.8; DB 20: Length 1543; |
| Best Local Similarity 70.7%; Pred No. 1.5e-15; |
| Matches 133; Conservative 0; Mismatches 52; Indels 3; Gaps 1 |
| QY 1 GTGAGCGTATCGATAAGCTTGATTCGAATTCGTGGATTGCAGCATTTAAAGCG 60 |
| DB |
| 657 GTCAAGGTTTCCAAGGTCGTGGTTCGATTTCCGTCGATTCGTCGATTTCAAAGCG 716 |
| QY 61 GTTACAACCTTAATAAAGAGAAAAAGAAGTTGAAGAAAAGGCTGA---GTAAGTAG 117 |
| DB |
| 717 ATTGACAGTTTCCGAAAAGAAAAAGAAAGATTGGAGAGAGGATGTAATTAATAAG 776 |
| QY 118 TATATAGTACAGACGAGAGATAGCCGCTCCTGATTCGTTAATTGAAGAAGAAGA 177 |
| DB |
| 777 TATATAGTATAGAACCGAGAGAGATAGCCGCTCCTGATTCGTTAATTAAGAAGAAAT 836 |
| QY 178 GCTCACCA 185 |
| DB |
| 837 GGTTTACA 844 |

RESULT 11
 AAD30982/c
 ID AAD30982 standard; DNA; 6215 BP.
 XX
 AC AAD30982;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE PBSNT27 vector containing N. tabacum chloroplast gene fragment.
 XX
 KW Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP;
 KM isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
 XX transgenic plant; tobacco; ds.
 XX
 OS Nicotiana tabacum.
 XX
 PN MO200210398-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001; 2001MO-US24037.
 XX
 PR 31-JUL-2000; 2000US-221703P.
 XX
 PA (HAHN/) HAHN F M.
 XX (KUEH/) KUEHNLE A R.
 XX
 PI Hahn FM, Kuehnle AR;
 XX
 DR WPI: 2002-217122/27.
 XX
 PT Use of specific genes of mevalonate and isoprenoid biosynthetic
 PT pathways, for providing a cell with herbicide or antibiotic resistance,
 PT and for providing transformed cells having increased isoprenoid
 PT production
 XX
 PS Example 9; Page 100-103; 193pp; English.
 XX
 CC The invention relates to the use of specific genes of the mevalonate
 CC and isoprenoid biosynthetic pathways and inactive gene sites
 CC (pseudogene). Genes of the invention are used to enhance biosynthesis
 CC of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)
 CC and isoprenoid pathway derived products in the plastids of transgenic
 CC plants and microalgae, for producing herbicide or antibiotic resistant
 CC transgenic plants and microalgae, for providing transformed cells with
 CC increased isoprenoid production compared to non-transformed cells, and
 CC for providing a cell with an inserted polynucleotide sequence encoding
 CC one or more products of interest. The present sequence is PBSNT27
 CC vector containing Nicotiana tabacum chloroplast gene fragment. This
 CC vector is used in the exemplification of the invention.
 XX
 SQ Sequence 6215 BP; 1667 A; 1396 C; 1268 G; 1884 T; 0 other;
 XX
 Query Match 23.1%; Score 43.4; DB 24; Length 6215;
 Best Local Similarity 57.9%; Pred. No. 0.015;
 Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 XX
 QY 1 GTGCAGCGTATCGATAGCTGATATCGAATCGTCGATTGGTTCGACATTAAAGCG 60
 DB 5542 GTGCAGCGTATCGATAGCTGATATCGAATCGTCGACCGCGGGGATCCCTGAAAT 5483
 QY 61 GTTGACAACCTTTAAAGAGAAAAAGAGTTGAAGAAAGGCTGTAGTAAGTAT 120
 DB 5482 TGGGTAGCTGTGTAAACCGGTCGATCTTATGAATGGTGGAGTACAGAAAT 5423
 QY 121 AAGTACAGACCGG 133
 DB 5422 ATAGCCAGAAAGG 5410
 RESULT 12
 AAD31038/c
 ID AAD31038 standard; DNA; 7252 BP.

XX
 AC AAD31038;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Plasmid transformation vector pRK07 DNA.
 XX
 KW Mevalonate; isopentenyl diphosphate; herbicide resistance; DMAPP; IPP;
 KM isoprenoid; dimethylallyl diphosphate; antibiotic resistance; enzyme;
 KM transgenic plant; yeast; phosphomevalonate kinase; HMGR; HMGS; AACCT;
 KM mevalonate kinase; mevalonate diphosphate decarboxylase; HMG-CoA; MDD;
 KM acetoacetyl thiolase; 3-hydroxy-3-methylglutaryl-coenzyme A synthase;
 KM MVK; PMK; HMG-CoA reductase; IPP isomerase; IPPi; ds.
 XX
 OS Chimeric - Saccharomyces cerevisiae.
 OS Chimeric - Arabidopsis thaliana.
 OS Chimeric - Rhodobacter capsulatus.
 XX
 PN MO200210398-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 31-JUL-2001; 2001MO-US24037.
 XX
 PR 31-JUL-2000; 2000US-221703P.
 XX
 PA (HAHN/) HAHN F M.
 XX (KUEH/) KUEHNLE A R.
 XX
 PI Hahn FM, Kuehnle AR;
 XX
 DR WPI: 2002-217122/27.
 XX
 PT Use of specific genes of mevalonate and isoprenoid biosynthetic
 PT pathways, for providing a cell with herbicide or antibiotic resistance,
 PT and for providing transformed cells having increased isoprenoid
 PT production
 XX
 PS Claim 77; Page 169-173; 193pp; English.
 XX
 CC The invention relates to the use of specific genes of the mevalonate
 CC and isoprenoid biosynthetic pathways and inactive gene sites
 CC (pseudogene). Genes of the invention are used to enhance biosynthesis
 CC of isopentenyl diphosphate (IPP), dimethylallyl diphosphate (DMAPP)
 CC and isoprenoid pathway derived products in the plastids of transgenic
 CC plants and microalgae, for producing herbicide or antibiotic resistant
 CC transgenic plants and microalgae, for providing transformed cells with
 CC increased isoprenoid production compared to non-transformed cells, and
 CC for providing a cell with an inserted polynucleotide sequence encoding
 CC one or more products of interest. The present sequence is plasmid
 CC transformation vector pRK07 containing operon C DNA which encodes the
 CC entire mevalonate pathway. This operon contains S. cerevisiae orfs
 CC encoding phosphomevalonate kinase (PMK), mevalonate kinase (MVK),
 CC mevalonate diphosphate decarboxylase (MDD), acetoacetyl thiolase (AACCT),
 CC A. thaliana orfs encoding 3-hydroxy-3-methylglutaryl-coenzyme A
 CC (HMG-CoA) synthase (HMGS), HMG-CoA reductase (HMGR) and R. capsulatus
 CC orf encoding IPP isomerase (IPPI).
 XX
 SQ Sequence 7252 BP; 1820 A; 1719 C; 1653 G; 2060 T; 0 other;
 XX
 Query Match 23.1%; Score 43.4; DB 24; Length 7252;
 Best Local Similarity 57.9%; Pred. No. 0.015;
 Matches 77; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
 XX
 QY 1 GTGCAGCGTATCGATAGCTGATATCGAATCGTCGATTGGTTCGACATTAAAGCG 60
 DB 6579 GTGCAGCGTATCGATAGCTGATATCGAATCGTCGACCGCGGGGATCCCTGAAAT 6520
 QY 61 GTTGACAACCTTTAAAGAGAAAAAGAGTTGAAGAAAGGCTGTAGTAAGTAT 120
 DB 6519 TGGGTAGCTGTGTAAACCGGTCGATCTTATGAATGGTGGAGTACAGAAAT 6460
 QY 121 AAGTACAGACCGG 133

| | | | | | | |
|----|------|------|------|---|--------------------|-------------------|
| 1 | 88.8 | 47.2 | 1543 | 4 | US-09-359-301A-9 | Sequence 9, Appl1 |
| 2 | 39 | 20.7 | 7218 | 1 | US-08-232-463-14 | Sequence 14, App |
| 3 | 38.8 | 20.6 | 4102 | 4 | US-09-402-266B-10 | Sequence 20, App |
| 4 | 37.8 | 20.1 | 1094 | 3 | US-09-144-918-3 | Sequence 3, Appl |
| 5 | 37.6 | 20.0 | 516 | 3 | US-08-928-799A-4 | Sequence 4, Appl1 |
| 6 | 37.6 | 20.0 | 1400 | 2 | US-08-553-367A-5 | Sequence 5, Appl1 |
| 7 | 37.6 | 20.0 | 1400 | 3 | US-09-295-306-5 | Sequence 5, Appl1 |
| 8 | 37.6 | 20.0 | 1490 | 4 | US-09-734-719-5 | Sequence 5, Appl1 |
| 9 | 36.4 | 19.4 | 821 | 3 | US-08-352-902D-146 | Sequence 16, Appl |
| 10 | 36.2 | 19.3 | 474 | 3 | US-08-928-299A-2 | Sequence 2, Appl1 |
| 11 | 35.6 | 18.9 | 1638 | 2 | US-08-838-219B-8 | Sequence 8, Appl1 |
| 12 | 35.6 | 18.9 | 1638 | 2 | US-09-233-335A-8 | Sequence 8, Appl1 |
| 13 | 35.6 | 18.9 | 1638 | 3 | US-09-233-335A-8 | Sequence 8, Appl1 |
| 14 | 35.6 | 18.9 | 1638 | 3 | US-09-402-036-8 | Sequence 8, Appl1 |
| 15 | 35.6 | 18.9 | 1638 | 4 | US-09-904-226-8 | Sequence 8, Appl1 |
| 16 | 35.4 | 18.8 | 1209 | 1 | US-07-750-0870A-2 | Sequence 8, Appl1 |
| 17 | 35.4 | 18.8 | 1209 | 1 | US-08-651-472-22 | Sequence 22, Appl |
| 18 | 35.4 | 18.8 | 1209 | 3 | US-08-356-928-22 | Sequence 22, App |
| 19 | 35.4 | 18.8 | 1618 | 1 | US-07-885-970A-22 | Sequence 22, App |
| 20 | 35.4 | 18.8 | 1618 | 1 | US-08-296-687A-22 | Sequence 22, Appl |
| 21 | 35.4 | 18.8 | 1518 | 1 | US-08-299-829-22 | Sequence 22, Appl |
| 22 | 35.4 | 18.8 | 5532 | 3 | US-08-621-472-72 | Sequence 72, Appl |
| 23 | 35.4 | 18.8 | 5532 | 3 | US-08-356-928-72 | Sequence 72, Appl |
| 24 | 35.4 | 18.8 | 6811 | 3 | US-08-651-472-67 | Sequence 67, App |
| 25 | 35.4 | 18.8 | 6811 | 3 | US-08-356-928-67 | Sequence 67, Appl |
| 26 | 35.4 | 18.8 | 7560 | 3 | US-09-103-478-4 | Sequence 4, Appl1 |
| 27 | 35.4 | 18.8 | 7560 | 4 | US-09-193-931C-4 | Sequence 4, Appl1 |

| | | | | | |
|----|------|--------|---|-------------------|---------------------|
| 28 | 18.8 | 756.0 | 4 | US-09-026-221-4 | Sequence 4, Appl 1 |
| 29 | 35.4 | 2126.2 | 4 | US-08-789-354-1 | Sequence 1, Appl 1 |
| 30 | 18.6 | 2126.3 | 3 | US-09-110-937-1 | Sequence 1, Appl 1 |
| 31 | 18.6 | 2126.3 | 3 | US-09-058-728B-1 | Sequence 1, Appl 1 |
| 32 | 18.6 | 2126.3 | 3 | US-09-232-857-1 | Sequence 1, Appl 1 |
| 33 | 35.3 | 2760.4 | 4 | US-09-904-645-30 | Sequence 30, Appl 1 |
| 34 | 34.8 | 888.4 | 4 | US-09-123-911-91 | Sequence 91, Appl 1 |
| 35 | 34.8 | 888.4 | 4 | US-09-643-597-91 | Sequence 91, Appl 1 |
| 36 | 34.8 | 888.4 | 4 | US-09-640-884A-91 | Sequence 91, Appl 1 |
| 37 | 34.8 | 888.4 | 4 | US-09-542-615A-91 | Sequence 91, Appl 1 |
| 38 | 18.5 | 858.4 | 4 | US-09-606-421B-91 | Sequence 91, Appl 1 |
| 39 | 34.8 | 1840.3 | 3 | US-09-065-047-12 | Sequence 12, Appl 1 |
| 40 | 18.5 | 1843.4 | 4 | US-09-066-047-12 | Sequence 12, Appl 1 |
| 41 | 34.8 | 3481.4 | 4 | US-09-462-645C-11 | Sequence 11, Appl 1 |
| 42 | 34.8 | 3481.4 | 4 | US-09-462-645C-7 | Sequence 7, Appl 1 |
| 43 | 34.8 | 4434.3 | 4 | US-08-815-809-1 | Sequence 1, Appl 1 |
| 44 | 34.8 | 4472.2 | 3 | US-08-816-158B-3 | Sequence 3, Appl 1 |
| 45 | 34.8 | 4472.3 | 3 | US-09-079-587-3 | Sequence 3, Appl 1 |

ALIGNMENTS

```

RESULT 1
US-09-359-301A-9
; Sequence 9, Application US/09359301A
; Patent No. 6426185
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Monto H.
; APPLICANT: della-Cioppa, Guy R.
; APPLICANT: Erwin, Robert L.
; APPLICANT: McGee, David R.
; TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A
; TITLE OF INVENTION: TRAIT IN A PLANT BY TRANSECTING A NUCLEIC ACID SEQUENCE OF
; TITLE OF INVENTION: A DONOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE
; FILE REFERENCE: 008010137US04
; CURRENT APPLICATION NUMBER: US/09/359,301A
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Rhdgrass mosaic virus
US-09-359-301A-9

Query Match
Best Local Similarity 47.2%; Score 88.8; DB 4; Length 1543;
Matches 133; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 1 GTCGACGGATCGATAGCTTGATATGCAATTCGTCGATTCGGTTGCACACATTAAAGCG 60
DB 657 GTCGACGGATTCGAAGGTGTGGTTGACGATTCGTCGATTCGGTTGCACACATTAAAGCG 716
QY 61 GTTGACAACCTTTAAAAAGGAAGAAAAAGAAAGTTGGAAGAAAGCGTGA---GTAACTAG 117
DB 717 ATTGAACAGTTCCGAAAGAAAAAGAAAAAGAAAGATTGGAGGAAGGATTAATTAATTAAG 776
QY 118 TATAATACAGACCGGAGAGATACGCCGCTCGATTCGTTAAATTGGAAGAAAGAAAGA 177
DB 777 TATAGATATAGACCGGAGAGATACGCCGCTCGATTCGTTCAATATTAAGAGAAATAT 836
QY 178 GCTCACCA 185
DB 837 GGTTCACA 844

RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

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```
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ. ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT29pt-Fls
US-08-232-463-14

Query Match
Best Local Similarity 20.7%; Score 39; DB 1; Length 7218;
Matches 24; Conservative 83; Mismatches 58; Indels 0; Gaps 0;

QY 14 AATAAGCTGATATCGAATTCGTCGATTCGTTGACAGCAATTTAAAGCGGTGACAACTTTA 73
DB 1480 ATTACTATCTATGCAAGTAGTAAAGAGATAGTAAGTAATTTGTCACRRRRRRRRRRRR 1421
QY 74 AAGAAGGAAAAAGAGAGTGAAGAAAGCGTGTAGTAAAGTAAAGTACAGTACAGACCGG 133
DB 1420 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1361
QY 134 AGAAGTACGCCGCTGCTGATTCGTTAAATTTGAAGAAGAGAGG 178
DB 1360 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1316

RESULT 3
US-09-402-266B-20/c
Sequence 20, Application US/09402266B
Patent No. 6537767
GENERAL INFORMATION:
APPLICANT: HINNEN, Albert
APPLICANT: HEGEMANN, Johannes
APPLICANT: MUNDER, Thomas
APPLICANT: SCHUSTER, Tilmer
APPLICANT: FELDMANN, Horst
APPLICANT: KRAMER, Walfried
APPLICANT: ZIMMERMANN, Friedrich
```

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APPLICANT: ENTIAN, Karl-Dieter
TITLE OF INVENTION: Process for Screening Antimycotically Active Substances
FILE REFERENCE: 38005-0094
CURRENT APPLICATION NUMBER: US/09/402,266B
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: PCT/EP98/01904
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: DE 19713572.2
PRIOR FILING DATE: 1997-04-02
SOFTWARE: Patentin version 3.0
SEQ. ID NO 20
LENGTH: 4102
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc.feature
LOCATION: ( )..( )
OTHER INFORMATION: Synthetic sequence
US-09-402-266B-20

Query Match
Best Local Similarity 20.6%; Score 38.8; DB 4; Length 4102;
Matches 76; Conservative 0; Mismatches 42; Indels 2; Gaps 1;

QY 1 GTGACGGTATGATAGCTTGATATCGAATTCGTCGATTCGTTGACGATTTAAAGCG 60
DB 1876 GTGACGGTATGATAGCTTGATATCGAATTCGTCGACGGCCGCAACATGAGAAATTG 1817
QY 61 GTTGACAACTTTAAAGAGAAAGAGTGAAGAAAGGCTGAGTAAGTAAGTAT 120
DB 1816 GGTAAATACGT--ATTAATTAATTAATGAACTTAATTGTGAGTTAGTATACATGCA 1759

RESULT 4
US-09-144-918-3/c
Sequence 3, Application US/09144918
Patent No. 6287807
GENERAL INFORMATION:
APPLICANT: KALLIS, Nicola G.
TITLE OF INVENTION: Muir
FILE REFERENCE: GMI0098
CURRENT APPLICATION NUMBER: US/09/144,918
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 60/060,682
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1094
TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: CDS
LOCATION: (497)...(1094)
US-09-144-918-3

Query Match
Best Local Similarity 20.1%; Score 37.8; DB 3; Length 1094;
Matches 45; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GTGACGGTATGATAGCTTGATATCGAATTCGTCGATTCGTTGACGATTTAA 57
DB 1062 GTGACGGTATGATAGCTTGATATCGAATTCGTCGACCGCGCATTTTCA 1006

RESULT 5
US-08-928-799A-4
Sequence 4, Application US/08928799A
Patent No. 6069302
GENERAL INFORMATION:
APPLICANT: Osborn, Thomas C
APPLICANT: Buttrille, David V
```

TITLE OF INVENTION: Hybrid Spring Oilseed Brassica napus
TITLE OF INVENTION: With Winter Germplasm Introgression
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plinckney St
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,799A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296, 94240
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Brassica napus
IMMEDIATE SOURCE:
CLONE: W67B3.77
FEATURE:
NAME/KEY: primer_bind
LOCATION: 358...377
US-08-928-799A-4

Query Match 20.0%; Score 37.6; DB 3; Length 516;
Best Local Similarity 72.1%; Pred. No. 0.018;
Matches 49; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GTCGACGGTATCGATATCGAATTCGTCGATTCGGTGCAGCATTTAAAGCG 60
|||||
Db 22 GTCGACGGTATCGATATCGAATTCGTCGATTCGGTGCAGCATTTAAAGCG 81
61 GTTGACAA 68
|||||
Db 82 GACACAA 89

RESULT 6
US-08-553-367A-5
Sequence 5, Application US/08553367A
Patent No. 5939539
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA-20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 5939539ember 27, 1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/FD4.5M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: PAT2353
US-08-553-367A-5

Query Match 20.0%; Score 37.6; DB 2; Length 1490;
Best Local Similarity 65.5%; Pred. No. 0.025;
Matches 55; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 7 GGATCGATAGCTGATATCGAATTCGTCGATTCGGTGCAGCATTTAAAGCGGTGAC 66
|||||
Db 1 GGATCGATAGCTGATATCGAATTCGTCGATTCGGTGCAGCATTTAAAGCGGTGAC 60
QY 67 AACTTTAAGAAGAAAGAAAG 90
|||||
Db 61 CTTCTGAGAAAAAGAAAG 84

RESULT 7
US-09-295-306-5
Sequence 5, Application US/09295306
Patent No. 6198021
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA-20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6198021ember 27, 1995
ATTORNEY/AGENT INFORMATION:

TELECOMMUNICATION INFORMATION
TELEPHONE: 202-721-8200

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cDNA
POSITION IN GENOME:
MAP POSITION: Human Chromosome 7q
SEQUENCE DESCRIPTION: SEQ ID NO: 146
US-08-352-902D-146

Query Match 19.4%; Score 36.4; DB 3; Length 821;
Best Local Similarity 97.4%; Pred. No. 0.048;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGACGGTATCGATACCTGATATCGAATTCGCGA 38
DB 12 GTGACGGTATCGATACCTGATATCGAATTCGCGA 49

RESULT 10

US-08-928-799A-2
Sequence 2, Application US/08928799A
Patent No. 6069302

GENERAL INFORMATION:

APPLICANT: Osborn, Thomas C
TITLE OF INVENTION: Hybrid Spring Oilseed Brassica napus
TITLE OF INVENTION: With Winter Germplasm Introgression
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pluckney St
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,799A
FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Beeson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296.94240
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 474 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Brassica napus

IMMEDIATE SOURCE:

CLONE: W6B10.T7

FEATURE:

NAME/KEY: primer blind

LOCATION: 146..165

US-08-928-799A-2

Query Match 19.3%; Score 36.2; DB 3; Length 474;
Best Local Similarity 77.2%; Pred. No. 0.047;
Matches 44; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GTGACGGTATCGATACCTGATATCGAATTCGCGATTGAGCACTTTAA 57
DB 23 GTGACGGTATCGATACCTGATATCGAATTCGCGATTGAGCACTTTGAA 79

RESULT 11
US-08-838-219B-8/C
Sequence 8, Application US/08838219B
Patent No. 5877012

GENERAL INFORMATION:

APPLICANT: Warren, Gregory M
APPLICANT: Kozietel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B

TITLE OF INVENTION: A No. 5877012el Class of Proteins for the

TITLE OF INVENTION: Control of Plant Pests

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: NY

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,219B

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/463,483

FILING DATE: 06-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,594

FILING DATE: 09-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/218,018

FILING DATE: 23-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40,403

REFERENCE/DOCKET NUMBER: CGC 1925

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8689

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1638 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 2..1191

OTHER INFORMATION: /Product- "Translation of cDNA

OTHER INFORMATION: encoding VIP3a(a) receptor"

US-08-838-219B-8

Query Match 18.9%; Score 35.6; DB 2; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GTGACGGTATCGATACCTGATATCGAATTCGCGATTGAGCACTTTAAAGCG 60

Db 1633 GTGACGCGTATCGATTAAGCTTGATATCGAATTCGCGGCGGCTGACATTTTTTTTCT 1574

OY 61 GTTGACAACTTTAA 74

Db 1573 CTTATAAATTTTTTA 1560

RESULT 12

US-09-233-336A-8/c
Sequence 8, Application US/09233336A
Patent No. 6107279

GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalin M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: A No. 6107279el Class of Proteins for the
TITLE OF INVENTION: Control of Plant Pests
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,336A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,219
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1925
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1191
OTHER INFORMATION: /product= "Translation of cDNA
OTHER INFORMATION: encoding VIP3a(a) receptor"

US-09-233-336A-8

| | | | | |
|--------------------------|-------|----------------|-----------|--------------|
| Query Match | 18.9% | Score 35.6; | DB 3; | Length 1638; |
| Best Local Similarity | 67.6% | Pred. NO. 0.1; | | |
| Matches 50; Conservative | 0; | Mismatches 24; | Indels 0; | Gaps 0; |

| | | | | |
|----|--|------|---|------|
| QY | | 1 | GTCACGCGTATCCGAATAGCTTGATATCGAATTCGGATTCGGTTGCACGACTTTAAACG | 60 |
| | | | | |
| | | | | |
| Dδ | | 1633 | GTCACGCGTATCCGAATAGCTTGATATCGAATTCGGATTCGGTTGCACGACTTTTCT | 1578 |
| | | | | |
| | | | | |
| QY | | 61 | GTCGCAACTTAA | 74 |
| | | | | |
| | | | | |
| Dδ | | 1573 | CTTATAATT | 1560 |

RESULT 13

US-09-233-72A-B/C
Sequence 8, Application US/09233752A
Patent No. 6137033

GENERAL INFORMATION:

APPLICANT: Warren, Gregory W
APPLICANT: Kozziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: A No. 6137033el Class of Proteins for the
NUMBER OF INVENTION: Control of Plant Pests
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,752A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/838,219
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1925
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1191
OTHER INFORMATION: /product- "translation of CDNA
US-09-233-752A-8 encoding VIP3A(a) receptor"

Query Match 18.9%; Score 35.6; DB 3; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1 GTCGACGGTATCGATTAAGCTTGATATCGAATTCGTCGATTCGGTTCGACCATTTAAAGCG 60
DB 1633 GTCGACGGTATCGATTAAGCTTGATATCGAATTCGCGCGCGCTGACCTTTTCTTTTCT 1574
OY 61 GTTGACAACCTTAA 74
DB 1573 CTTATTAATTTTAA 1560

RESULT 14
US-09-402-036-8/c
Sequence 8, Application US/09402036
Patent No. 6291156
GENERAL INFORMATION:
APPLICANT: Estruch, Juan J.
APPLICANT: Yu, Cao-Guo
APPLICANT: Warren, Gregory W.
APPLICANT: Desai, Nalini
APPLICANT: Koziel, Michael
APPLICANT: Nye, Gordon
TITLE OF INVENTION: Plant Pest Control
FILE REFERENCE: S-21284C
CURRENT APPLICATION NUMBER: US/09/402,036
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: PCT/EP98/01952
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 08/838,219
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,263
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,265
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/463,483
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/314,594
PRIOR FILING DATE: 1994-09-09
PRIOR APPLICATION NUMBER: 08/218,018
PRIOR FILING DATE: 1994-03-24
PRIOR APPLICATION NUMBER: 08/037,057
PRIOR FILING DATE: 1993-03-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 8
LENGTH: 1638
TYPE: DNA
ORGANISM: Agrotis ipsilon
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1189)
OTHER INFORMATION: translation of CDNA encoding VIP3A(a) receptor
US-09-402-036-8

Query Match 18.9%; Score 35.6; DB 3; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1 GTCGACGGTATCGATTAAGCTTGATATCGAATTCGTCGATTCGGTTCGACCATTTAAAGCG 60
DB 1633 GTCGACGGTATCGATTAAGCTTGATATCGAATTCGCGCGCGCTGACCTTTTCTTTTCT 1574

OY 61 GTTGACAACCTTAA 74
DB 1573 CTTATTAATTTTAA 1560

RESULT 15
US-09-904-226-8/c
Sequence 8, Application US/09904226
Patent No. 6429360
GENERAL INFORMATION:
APPLICANT: Estruch, Juan J.
APPLICANT: Warren, Gregory W.
APPLICANT: Desai, Nalini
APPLICANT: Koziel, Michael
APPLICANT: Nye, Gordon
TITLE OF INVENTION: Plant Pest Control
FILE REFERENCE: S-21284D
CURRENT APPLICATION NUMBER: US/09/904,226
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/EP98/01952
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 08/838,219
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,263
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/832,265
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/463,483
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 08/314,594
PRIOR FILING DATE: 1994-09-09
PRIOR APPLICATION NUMBER: 08/218,018
PRIOR FILING DATE: 1994-03-24
PRIOR APPLICATION NUMBER: 08/037,057
PRIOR FILING DATE: 1993-03-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 8
LENGTH: 1638
TYPE: DNA
ORGANISM: Agrotis ipsilon
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(1189)
OTHER INFORMATION: translation of CDNA encoding VIP3A(a) receptor
US-09-904-226-8

Query Match 18.9%; Score 35.6; DB 4; Length 1638;
Best Local Similarity 67.6%; Pred. No. 0.1;
Matches 50; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1 GTCGACGGTATCGATTAAGCTTGATATCGAATTCGTCGATTCGGTTCGACCATTTAAAGCG 60
DB 1633 GTCGACGGTATCGATTAAGCTTGATATCGAATTCGCGCGCGCTGACCTTTTCTTTTCT 1574
OY 61 GTTGACAACCTTAA 74
DB 1573 CTTATTAATTTTAA 1560

Search completed: September 26, 2003, 10:16:57
Job time : 67 secs

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|------|----|------------------|-------------|------|
| 188 | 11 | US-09-758-962-1 | Sequence 1 | App1 |
| 181 | 11 | US-09-758-962-5 | Sequence 7 | App1 |
| 181 | 11 | US-09-758-962-7 | Sequence 7 | App1 |
| 180 | 11 | US-09-758-962-3 | Sequence 6 | App1 |
| 187 | 11 | US-09-758-962-3 | Sequence 3 | App1 |
| 151 | 11 | US-09-758-962-2 | Sequence 2 | App1 |
| 148 | 14 | US-10-165-420-2 | Sequence 2 | App1 |
| 796 | 12 | US-10-211-079-19 | Sequence 19 | App1 |
| 796 | 12 | US-10-356-708-18 | Sequence 18 | App1 |
| 799 | 12 | US-10-211-079-23 | Sequence 23 | App1 |
| 799 | 12 | US-10-356-708-22 | Sequence 22 | App1 |
| 808 | 12 | US-10-211-079-22 | Sequence 22 | App1 |
| 808 | 12 | US-10-356-708-21 | Sequence 21 | App1 |
| 1543 | 14 | US-10-236-938-17 | Sequence 17 | App1 |
| 1543 | 14 | US-10-133-934-9 | Sequence 9 | App1 |
| 1543 | 14 | US-10-105-697-9 | Sequence 9 | App1 |

| | | | | | | |
|----|------|------|-------|----|----------------------|---------------------|
| 17 | 88.8 | 47.2 | 1543 | 14 | US-10-120-530-9 | Sequence 9, Appl1 |
| 18 | 88.8 | 47.2 | 1543 | 14 | US-10-137-765-23 | Sequence 23, Appl1 |
| 19 | 88.8 | 47.2 | 1543 | 14 | US-10-166-337-23 | Sequence 23, Appl1 |
| 20 | 88.8 | 47.2 | 1543 | 14 | US-10-142-077-9 | Sequence 9, Appl1 |
| 21 | 81 | 43.1 | 1536 | 14 | US-10-072-338-31 | Sequence 31, Appl1 |
| 22 | 43.4 | 23.1 | 6215 | 11 | US-09-918-740-17 | Sequence 17, Appl1 |
| 23 | 43.4 | 23.1 | 7252 | 11 | US-09-918-740-73 | Sequence 73, Appl1 |
| 24 | 43.4 | 23.1 | 7252 | 11 | US-09-918-740-75 | Sequence 75, Appl1 |
| 25 | 40.2 | 22.4 | 13917 | 11 | US-09-918-740-75 | Sequence 75, Appl1 |
| 26 | 40.2 | 22.4 | 526 | 10 | US-09-924-035A-40-72 | Sequence 72, Appl1 |
| 27 | 39.8 | 21.2 | 526 | 10 | US-09-924-035A-430 | Sequence 430, Appl1 |
| 28 | 39.2 | 20.9 | 327 | 10 | US-09-924-035A-634 | Sequence 634, Appl1 |
| 29 | 39 | 20.7 | 456 | 12 | US-09-924-035A-52 | Sequence 52, Appl1 |
| 30 | 38.4 | 20.4 | 382 | 10 | US-09-814-353-15014 | Sequence 15014, A |
| 31 | 38.4 | 20.4 | 781 | 14 | US-10-198-846-720 | Sequence 720, Appl1 |
| 32 | 38 | 20.2 | 434 | 10 | US-09-924-035A-656 | Sequence 4407, A |
| 33 | 38 | 20.2 | 465 | 10 | US-09-924-035A-730 | Sequence 656, Appl1 |
| 34 | 38 | 20.2 | 616 | 11 | US-09-776-724A-62 | Sequence 730, Appl1 |
| 35 | 37.8 | 20.1 | 122 | 11 | US-09-758-962-4 | Sequence 62, Appl1 |
| 36 | 37.8 | 20.1 | 587 | 14 | US-10-144-829-35 | Sequence 4, Appl1 |
| 37 | 37.8 | 20.1 | 1094 | 10 | US-09-932-818-3 | Sequence 35, Appl1 |
| 38 | 37.4 | 19.9 | 319 | 12 | US-09-814-353-13335 | Sequence 3, Appl1 |
| 39 | 37.4 | 19.9 | 458 | 12 | US-09-814-353-13302 | Sequence 13335, A |
| 40 | 37 | 19.5 | 4941 | 13 | US-10-001-189-53 | Sequence 13302, A |
| 41 | 36.6 | 19.5 | 148 | 7 | US-08-935-377-7 | Sequence 53, Appl1 |
| 42 | 36.6 | 19.5 | 148 | 7 | US-09-822-220-7 | Sequence 7, Appl1 |
| 43 | 36.6 | 19.5 | 148 | 10 | US-09-987-456-3 | Sequence 3, Appl1 |
| 44 | 36.6 | 19.5 | 148 | 11 | US-09-818-991-5 | Sequence 5, Appl1 |
| 45 | 36.6 | 19.5 | 148 | 14 | US-10-052-942-152 | Sequence 152, Appl1 |

ALIGNMENTS

```

RESULT 1
US-09-758-962-1
: Sequence 1, Application US/09758962
: Publication No. US20030049228A1
: GENERAL INFORMATION:
: APPLICANT: SANTA CRUZ, SIMON
: APPLICANT: TOTI, RACHAEL L.
: APPLICANT: CHAPMAN, SEAN
: APPLICANT: CARR, FIONA
: APPLICANT: POGDE, GREGORY
: TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
: TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTORS
: FILE REFERENCE: 008010192NPUSO
: CURRENT APPLICATION NUMBER: US/09/758,962
: CURRENT FILING DATE: 2001-01-09
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 188
: TYPE: DNA
: ORGANISM: Potato virus
: US-09-758-962-1

```

[illegible]

| | | | |
|----|-----|----------|-----|
| Oy | 181 | CACCATGG | 188 |
| | | | |
| Db | 181 | CACCATGG | 188 |

RESULT 2
MS-09-75

```

Sequence 5, Application US/09758962
Publication No. US20030049228A1
GENERAL INFORMATION:
APPLICANT: SANTA CRUZ, SIMON
APPLICANT: TOTH, RACHAEL L.
APPLICANT: CHAPMAN, SEAN
APPLICANT: CARR, FIONA
APPLICANT: POGUE, GREGORY
TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTORS
FILE REFERENCE: 008010192NPUS00
CURRENT APPLICATION NUMBER: US/09/758,962
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ. ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO. 5
LENGTH: 181
TYPE: DNA
ORGANISM: Potato virus
US-09-758-962-5

```

| | | | | |
|---------------------------|--------|--------------------|--------|------------------|
| Query Match | 96.3% | Score 181; | DB 11; | Length 181; |
| Best Local Similarity | 100.0% | Pred. No. 1,4e-41; | | |
| Matches 181; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0 |

| | | | |
|----|-----|---|-----|
| QY | 1 | GTGCACGGGATGGAATTAAGCTTGATTCGAATTCGCGATTCGGTGGAGCATTTAAAGCG | 60 |
| | | | |
| Db | 1 | GTGCACGGGATCGATTAAGCTTGATTCGAATTCGCGATTCGGTGGAGCATTTAAAGCG | 60 |
| | | | |
| QY | 61 | GTTCACAACTTTAAAGAAGGAAAAAGAAGTTGAGAAAAAGCGCTGAGTAAGTAAGTAT | 120 |
| | | | |
| Db | 61 | GTTCACAACTTTAAAGAAGGAAAAAGAAGTTGAGAAAAAGCGCTGAGTAAGTAAGTAT | 120 |
| | | | |
| QY | 121 | AAGTACACAGCCGGAGAAATACGCCGGCTCTATTCGTTAATTTGAAAGAAAGAGCT | 180 |
| | | | |
| Db | 121 | AAGTACACAGCCGGAGAAATACGCCGGCTCTATTCGTTAATTTGAAAGAAAGAGCT | 180 |
| | | | |
| QY | 181 | C 181 | |
| | | | |
| Db | 181 | C 181 | |
| | | | |

RESULT 3
US-09-751

```

Sequence 7, Application US/09758962
Publication No. US2003004928A1
GENERAL INFORMATION:
APPLICANT: SANTA CRUZ, SIMON
APPLICANT: TOTH, RACHAEL L.
APPLICANT: CHAPMAN, SEAN
APPLICANT: CARR, ETONA
APPLICANT: FOGUE, GREGORY
TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTORS
FILE REFERENCE: 008010192NPUS00
CURRENT APPLICATION NUMBER: US/09/7758,962
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 181
TYPE: DNA
ORGANISM: Potato virus
US-09-758-962-7

```

| Query Match | 87.88; Score 165; DB 11; Length 181; |
|-------------|--------------------------------------|
|-------------|--------------------------------------|

Best Local Similarity 94.5%; Pred. NO. 4.7e-37;
Matches 171; conservative 0; Mismatches 10; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | GTCGACGGTATCGATTAAGCTTCAATTCGAAATTCGCAATTCGGTATTCGACGACATTTAAAGCG | 60 |
| Db | 1 | GTCGACGGTATCGATTAAGCTTCAATTCGAAATTCGCAATTCGGTATTCGACGACATTTAAAGCG | 60 |
| QY | 61 | GTTGACMACTTTAAAAAGAGAAAAAGAGGTTGAGAAAAAGGTGTAAGTAACTAAGTAT | 120 |
| Db | 61 | GTTGACGACCTTTAAAAAGAGAAAAAGAGGTTGAGAAAAAGGAGTAACTAAGTAACTAAGTAT | 120 |
| QY | 121 | AAGTACAGACCGGAGAGTACGCCGCTCTCTGATTGCTTTAATTGGAAGAAGAAAGACT | 180 |
| Db | 121 | AAGTACAGACCGGAGAGAGCAGCCGCTCTCTGATACGTTTAATTGGAAGAAGAGCAGAGCT | 180 |
| QY | 181 | C | 181 |
| Db | 181 | C | 181 |

RESULT 4

```

1 // Sequence 6, Application US/09758962
2 // Publication No. US20030049228A1
3 // GENERAL INFORMATION:
4 // APPLICANT: SANTA CRUZ, SIMON
5 // APPLICANT: TOTM, RACHAEL L.
6 // APPLICANT: CHAPMAN, SEAN
7 // APPLICANT: CARR, FIONA
8 // APPLICANT: POGUE, GREGORY
9 // TITLE OF INVENTION: A NOVEL STRATEGY FOR THE EXPRESSION OF
10 // TITLE OF INVENTION: FOREIGN GENES FROM PLANT VIRUS VECTORS
11 // FILL REFERENCE: 008010192NPUS00
12 // CURRENT APPLICATION NUMBER: US/09/758,962
13 // CURRENT FILING DATE: 2001-01-09
14 // NUMBER OF SEQ ID NOS: 8
15 // SOFTWARE: FastSeq for Windows Version 4.0
16 // SEQ ID NO 6
17 // LENGTH: 180
18 // TYPE: DNA
19 // ORGANISM: Potato virus
20 // US-09-758-962-6

```

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 80.5% | Score 151.4; | DB 11; | Length 180; |
| Best Local Similarity | 93.4% | Pred. NO. 3.2e-33; | | |
| Matches 169; Conservative | 0; | Mismatches 11; | Indels 1; | Gaps 1; |

| | | | |
|----|-----|---|-----|
| QY | 1 | GTGCGAGGATGATGATAGCTTGATATCGAAATGTCGATCGGTGCGACGATTTAAACG | 60 |
| Db | 1 | GTGCGAGGATGATGATAGCTTGATATCGAAATGTCGATCGGTGCGACGATTTAAACG | 59 |
| QY | 61 | GTTCACACCTTTAAAAGAAAGAAAAAGAGTTGAAGAAAAAGCGTGTAGTAAGTAAT | 120 |
| Db | 60 | GTTCACACCTTTAAAAGAAAGAAAAAGAGTTGAAGAAAAAGCGTGTAGTAAGTAAT | 119 |
| QY | 121 | AGGTACACACCCGGAGAGTAGCGCCGCTCTGATTGCTTAATTGTAAGAAAGAAAGAGCT | 180 |
| Db | 120 | AGGTACACACCCGGAGAGTAGCGCCGCTCTGATTGCTTAATTGTAAGAAAGAAAGAGCT | 179 |
| QY | 181 | C | 181 |
| Db | 180 | C | 180 |

RESULT 5

US-05-09-758-662-3/c
Sequence 3, Application US/09758962
Publication No. US20030049228A1
GENERAL INFORMATION:
APPLICANT: SANTA CRUZ, SIMON
APPLICANT: TOTH, RACHAEL L.
APPLICANT: CHAPMAN, SEAN
APPLICANT: CARR, ETONA

QY
1 GTCCGCGGTATACGATTAAGCTTGATTCGATTGGTTCGACATTTAAACG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
544 GTCGAAGGTTTCGAGGCGTGTTGACCATTTCTGCATTTGGTCGACATTTAAAGC 603
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY
61 GTTCACAATTTAAAGAAGAAAAGAAGTTAAGAAAAAGGTGA---GTACTAG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 604 GTTGACACCTTCAGAAAGAAAAAGAAAGATTCGAGAGAAAGAGTCGTAATATATATATATAG 663

OY 118 TATAAGTACAGACCGGAGACAGTACCGCGCTCTATTCGTTTAATTGAAAGAAAGAA 175

Db 664 TTTCAGATATAGACCGGAGAGATACCGCGCTCAGCATTCGTTAAATTATATAAGAGAAAGAA 721

```

RESULT 9
US-10-356-708-18
; Sequence 18, Application US/10356708
; Publication No. US20030157682A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: MISMATCH ENONCODELEASES AND METHODS OF USE THEREOF
FILE REFERENCE: P-Lg 10100
CURRENT APPLICATION NUMBER: US/10/356,708
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,722
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 10/098,155
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 10/211,079
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Tobamovirus Cg
; US-10-356-708-18

```

| Query Match | 47.9% | Score 90 | DB 12 | Length 796 |
|-----------------------|----------------|---|----------|------------|
| Best Local Similarity | 73.0% | Pred. No. 1.1e-15 | | |
| Matches 130 | Conservative 0 | Mismatches 45 | Indels 3 | Gaps 1 |
| QY | 1 | GTGACGGTATCGATTAACTTGATATCGAAATTCGTCGATTCGGTTCACAGCATTTAAAGCG | 60 | |
| | | | | |
| DB | 544 | GTGACGAGGTTCGGAAGCGGTGGTGTGACGATTCGTGATTCGGTTCGACAGATTTCAAGCG | 603 | |
| | | | | |
| QY | 61 | GTTGCACTTTAAAGAGGAAAAAANAAGTTGAAAGAAAGCGTGA--GTAACTAG | 117 | |
| | | | | |
| DB | 604 | GTTGCACTTTCAAGAAAGAAAAAANAAGATTGGAGAAAGATTTAAATATATATAAG | 663 | |
| | | | | |
| QY | 118 | TATAGTTCACAGCCGAGAGTACGCCGCGTCTGATTCGTTTATTTGGAAGAGAAA | 175 | |
| | | | | |
| DB | 664 | TTTAGATTTAACCAGAGATACGCCGCGTTCAGAGATTCGTTAATATTTAAGAGAAA | 721 | |
| | | | | |

```

RESULT 10
US-10-211-079-23
; Sequence 23, Application US/10211079
; Publication No. US20030148315A1
; GENERAL INFORMATION:
; APPLICANT: Padgett, Hal S.
; APPLICANT: Vojdani, Andrew A.
; APPLICANT: Smit, Mark L.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding CEL I
; FILE REFERENCE: P-16 5381
; CURRENT APPLICATION NUMBER: US/10/211,079
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 10/098,155
; PRIOR FILING DATE: 2002-03-14
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 799
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-211-079-23

```

| | | | | | |
|----|-----------------------|--|-------------------|----------|------------|
| | Query Match | 47.9% | Score 90 | DB 12 | Length 799 |
| | Best Local Similarity | 73.0% | Pred. No. 1.1e-15 | | |
| | Matches 130 | Conservative 0 | Mismatches 45 | Indels 3 | Gaps 1 |
| Qy | 1 | GTGCGAGGTATCGATMACTTGATATTCATATTCGTCGATTCGCTGTCAGCATTTAAACGCG | 60 | | |
| | | | | | |
| | | | | | |
| | | | | | |
| Db | 547 | GTGCGAGGTTCGAAAGCGCGTGCGTTCACATTTTCGTCGATTCGGTCGACGCAATTCAGGCG | 606 | | |
| | | | | | |
| Qy | 61 | GTTGACAACTTTAAAGAGAGAAAAAGAGTTGAAGAAAAAGGTCGT---GTAAGTAAG | 117 | | |
| | | | | | |
| | | | | | |
| | | | | | |
| Db | 607 | GTTGACACTTTCAGAAAGAAAAAGAAAGGATGGAGAAAAAGAGTAAATATATATAG | 666 | | |
| | | | | | |
| | | | | | |
| | | | | | |
| Qy | 118 | TATAGTACAGACCGAGATAGACCGCGCTCGTATTCGTTTAATTGAAGAGAGAAA | 175 | | |
| | | | | | |
| | | | | | |
| | | | | | |
| Db | 667 | TTTGATATTACACCGAGAGATACCGCGCGTTCAGAGATTGCTTAATATATAAAGAGAGAA | 724 | | |

```

RESULT 11
US-10-356-708-22
; Sequence 22, Application US/10356708
; Publication No. US20030157682A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: MISMATCH ENDONUCLEASES AND METHODS OF USE THEREOF
; FILE REFERENCE: P-GG 10100
; CURRENT APPLICATION NUMBER: US/10/356,708
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353,722
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 10/098,155
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 10/721,079
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 22
; LENGTH: 799
; TYPE: DNA
; ORGANISM: Artificial Sequence derived from tomato mosaic virus and TMV-Cg
; FEATURE:
; OTHER INFORMATION: This sequence was derived by shuffling in accordance with the
US-10-356-708-22

```

| | Query Match | 47.98 | Score 90 | DB 12 | Length 799 |
|----|-----------------------|--|-------------------|---------------|------------|
| | Best Local Similarity | 73.08 | Pred. No. 1.1e-15 | | |
| | Matches 130 | Conservative | 0 | Mismatches 45 | Indels 3 |
| | | | | Gaps | 1 |
| QY | 1 | GTCGACGGTATACGTAAGCTGATATGCAATTCCTCGATTGGTGTGCGACATTTAAAGCG | 60 | | |
| Db | 547 | GTCGAAGTTTCGAAGCGCGTGGTGACGATTTCTCGATTGGTGTGCGACATTTAAAGCG | 606 | | |
| QY | 61 | GTTGACACATTTAAAGAAAGAAAAAGGTTGAAGAAAAAGGTGTGA--GTAAGTAG | 117 | | |
| Db | 607 | GTTGACACTTTCAGAAAGAAAAAGAAAGATTGAGAAAGATGTAATATTAATTAAG | 666 | | |
| QY | 118 | TATTAAGTACAGACCGGGAAGTAGTACCGCGGTCTTATTCGTTTAATTGGAAGAGAAA | 175 | | |
| Db | 667 | TTTATGATATATGACCGGAGAGATACCGCGGTCTGAGATTCGTTTAATTTAAGAGAGAAA | 724 | | |

RESULT 12
 US-10-211-079-22
 Sequence 22, Application US/10211079
 Publication No. US20030148315A1
 GENERAL INFORMATION:
 APPLICANT: Padgett, Hal S.
 APPLICANT: Vaesmongs, Andrew A.
 APPLICANT: Vojdani, Fahrieh S.
 APPLICANT: Smith, Mark L.
 TITLE OF INVENTION: Nucleic Acid Molecules Encoding CEL I
 Endonuclease and Methods of Use Thereof

```
FILE REFERENCE: P-LG 5381
CURRENT APPLICATION NUMBER: US/10/211,079
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 10/098,155
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 808
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic construct
US-10-211-079-22

Query Match
Best Local Similarity 73.0%; Score 90; DB 12; Length 808;
Matches 130; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

1 GTGACGGTATCGATAGCTGATATCGAATTCGTGATTCGGTTGACGATTTAAAGCG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
556 GTCGAAGGTTTCGAAGCGGTGGTGCATTTGCGATGCGTCGACGATTTCAAGCG 615
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GTTGACACTTTAAAGAGAGAAAAAGAGTTGAAGAAAGGTTGA--GTAAGTAAG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
616 GTTGACACTTTCAAGAGAAAAAGAGATTTGAGAGAAAGATGAATTAATTAAG 675
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 TATAAGTACAGACCGGAGAGATGCGGCTCCTGATTCGTTAATTGGAAGAGAAA 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
676 TTAGATATAGACCGGAGAGATGACCCGCTCAGATTCGTTAATTAATTAAGAGAAA 733
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-10-356-708-21
; Sequence 21, Application US/10356708
; Publication No. US20030157682A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: MISMATCH ENDONUCLEASES AND METHODS OF USE THEREOF
FILE REFERENCE: P-LG 10100
CURRENT APPLICATION NUMBER: US/10/356,708
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,722
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 10/098,155
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 10/211,079
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 808
TYPE: DNA
ORGANISM: Artificial Sequence derived from tomato mosaic virus and TMV-Cg
FEATURE:
OTHER INFORMATION: This sequence was derived by shuffling in accordance with the method of US-10-356-708-21
US-10-356-708-21

Query Match
Best Local Similarity 73.0%; Score 90; DB 12; Length 808;
Matches 130; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

1 GTGACGGTATCGATAGCTGATATCGAATTCGTGATTCGGTTGACGATTTAAAGCG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
556 GTCGAAGGTTTCGAAGCGGTGGTGCATTTGCGATGCGTCGACGATTTCAAGCG 615
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GTTGACACTTTAAAGAGAGAAAAAGAGTTGAAGAAAGGTTGA--GTAAGTAAG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
616 GTTGACACTTTCAAGAGAAAAAGAGATTTGAGAGAAAGATGAATTAATTAAG 675
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 TATAAGTACAGACCGGAGAGATGCGGCTCCTGATTCGTTAATTGGAAGAGAAA 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
DB 676 TTAGATATAGACCGGAGAGATGACCCGCTCAGATTCGTTAATTAATTAAGAGAAA 733

RESULT 14
US-10-236-508-17
; Sequence 17, Application US/10236508
; Publication No. US20030167512A1
GENERAL INFORMATION:
APPLICANT: Monto H. Kumagai
APPLICANT: Guy R. della-Cioppa
APPLICANT: Robert L. Erwin
APPLICANT: David R. McGee
TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY A
TITLE OF INVENTION: TRANSFECTING A NUCLEIC ACID SEQUENCE OF A DONOR PLANT INTO A
TITLE OF INVENTION: DIFFERENT HOST PLANT IN A POSITIVE ORIENTATION
FILE REFERENCE: 0080101370505
CURRENT APPLICATION NUMBER: US/10/236,508
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 1543
TYPE: DNA
ORGANISM: Ribgrass mosaic virus (RMV)
US-10-236-508-17

Query Match
Best Local Similarity 70.7%; Score 88.8; DB 12; Length 1543;
Matches 133; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

1 GTGACGGTATCGATAGCTGATATCGAATTCGTGATTCGGTTGACGATTTAAAGCG 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
657 GTCGAAGGTTTCGAAGCGGTGGTGCATTTGCGATGCGTCGATTCGATTTCAAGCG 716
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GTTGACACTTTAAAGAGAGAAAAAGAGTTGAAGAAAGGTTGA--GTAAGTAAG 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
717 ATTGACAGTTCCGAGAGAAAAAGAGAAAGATTTGAGAGAGGATGAATTAATTAAG 776
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 TATAAGTACAGACCGGAGAGATGCGGCTCCTGATTCGTTAATTGGAAGAGAAA 177
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
777 TATAAGTATAGACCGGAGAGATGACCCGCTCCTGATTCGTTAATTAATTAAGAGAAAAT 836
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 GTCACCA 185
| | | |
DB 837 GGTTTACA 844

RESULT 15
US-10-133-934-9
; Sequence 9, Application US/10133934
; Publication No. US20030024008A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Monto H.
APPLICANT: della-Cioppa, Guy R.
APPLICANT: Erwin, Robert L.
APPLICANT: McGee, David R.
TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A
TITLE OF INVENTION: TRAIT IN A PLANT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF A
TITLE OF INVENTION: TRANSFECTING A NUCLEIC ACID SEQUENCE OF A DONOR PLANT INTO A DIFFERENT HOST PLANT IN AN ANTI-SENSE
FILE REFERENCE: 0080101370504
CURRENT APPLICATION NUMBER: US/10/133,934
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US/09/359,301A
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1543
TYPE: DNA
ORGANISM: Ribgrass mosaic virus
US-10-133-934-9
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 08:29:44 ; Search time 2201 Seconds
(without alignments)
2075.984 Million cell updates/sec

Title: US-09-758-962-1

Perfect score: 188
Sequence: 1 gtcgacggtatcgataagct.....gaagaagagctcaccatg 188

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estb1:*
2: em_estb2:*
3: em_estb3:*
4: em_estb4:*
5: em_estb5:*
6: em_estb6:*
7: em_estb7:*
8: em_estb8:*
9: em_estb9:*
10: em_estb10:*
11: em_estb11:*
12: em_estb12:*
13: em_estb13:*
14: em_estb14:*
15: em_estb15:*
16: em_estb16:*
17: em_estb17:*
18: em_estb18:*
19: em_estb19:*
20: em_estb20:*
21: em_estb21:*
22: em_estb22:*
23: em_estb23:*
24: em_estb24:*
25: em_estb25:*
26: em_estb26:*
27: em_estb27:*
28: em_estb28:*
29: em_estb29:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 47.6 | 25.3 | 775 | 13 | BU745631 CH2#001.B |
| 2 | 44.8 | 23.5 | 790 | 14 | BU725337 SUMCD10 |
| 3 | 44.2 | 23.5 | 790 | 14 | BU725337 SUMCD10 |
| 4 | 44 | 23.4 | 234 | 9 | BU740521 BR110478 |

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 5 | 43.4 | 23.1 | 668 | 13 | BU791304 |
| 6 | 43.4 | 23.1 | 1017 | 29 | BU571990 |
| 7 | 43.4 | 23.1 | 1126 | 13 | BU745817 |
| 8 | 43.2 | 23.0 | 229 | 14 | BU69458 |
| 9 | 43.2 | 23.0 | 1092 | 29 | BU561465 |
| 10 | 42.8 | 22.8 | 269 | 13 | BU802512 |
| 11 | 42.8 | 22.8 | 270 | 13 | BU802512 |
| 12 | 42.8 | 22.6 | 1098 | 29 | BU556045 |
| 13 | 42.4 | 22.6 | 708 | 29 | BU549869 |
| 14 | 42.4 | 22.6 | 833 | 13 | BU744514 |
| 15 | 42.4 | 22.6 | 958 | 13 | BU745422 |
| 16 | 42.2 | 22.4 | 637 | 13 | BU715329 |
| 17 | 42.2 | 22.4 | 708 | 13 | BU723206 |
| 18 | 42.2 | 22.4 | 1036 | 13 | BU745781 |
| 19 | 42.2 | 22.4 | 1339 | 29 | BU556095 |
| 20 | 42.2 | 22.3 | 837 | 29 | BU574561 |
| 21 | 41.8 | 22.2 | 226 | 14 | BU71406 |
| 22 | 41.8 | 22.2 | 235 | 14 | BU71333 |
| 23 | 41.8 | 22.2 | 245 | 14 | BU71404 |
| 24 | 41.8 | 22.2 | 495 | 14 | BU71327 |
| 25 | 41.8 | 22.2 | 606 | 14 | BU71327 |
| 26 | 41.8 | 22.2 | 805 | 29 | BU553266 |
| 27 | 41.6 | 22.1 | 810 | 13 | BU751450 |
| 28 | 41.2 | 21.9 | 770 | 13 | BU751642 |
| 29 | 41.1 | 21.8 | 398 | 12 | BU751642 |
| 30 | 41.1 | 21.8 | 942 | 13 | BU746236 |
| 31 | 40.8 | 21.7 | 198 | 14 | BU746236 |
| 32 | 40.8 | 21.7 | 521 | 13 | BU802673 |
| 33 | 40.8 | 21.7 | 649 | 9 | BU186540 |
| 34 | 40.8 | 21.7 | 836 | 13 | BU746273 |
| 35 | 40.8 | 21.7 | 869 | 13 | BU751583 |
| 36 | 40.8 | 21.7 | 945 | 13 | BU749186 |
| 37 | 40.8 | 21.7 | 1614 | 29 | BU579281 |
| 38 | 40.6 | 21.6 | 299 | 13 | BU802171 |
| 39 | 40.6 | 21.6 | 574 | 13 | BU710691 |
| 40 | 40.6 | 21.6 | 574 | 13 | BU710879 |
| 41 | 40.6 | 21.6 | 575 | 13 | BU710850 |
| 42 | 40.6 | 21.6 | 651 | 29 | BU550551 |
| 43 | 40.6 | 21.6 | 709 | 13 | BU723792 |
| 44 | 40.6 | 21.6 | 778 | 29 | BU564926 |
| 45 | 40.6 | 21.6 | 833 | 13 | BU744547 |

ALIGNMENTS

RESULT 1
LOCUS BU745631
DEFINITION CH2#001_B09T3 Canine heart normalized cDNA library in pBluescript
ACCESSION BU745631
VERSION BU745631.1 GI:23695092
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 775)
Y.I., Desai, R., Olarte, M., Henthorn, P. and George A.L.
Expressed sequence tags from Canine heart
Unpublished
Other ESTs: CH2#001_B09T7
Contact: George A.L.
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: a1.george@vanderbilt.edu
Insert Length: 1622 Std Error: 0.00
Seq primer: T3: ATTAACTCCTCCTCAAGGA
High quality sequence start: 59

LOCUS AW740521 254 bp mRNA linear EST 27-APR-2000
 DEFINITION BR10478 Biomphalaria glabrata (BS-90)-unexposed lambda Zap Library
 ACCESSION Biomphalaria glabrata cDNA clone RBGIG267R, mRNA sequence.
 AW740521
 VERSION AW740521.1 GI:7651614
 KEYWORDS EST
 SOURCE Biomphalaria glabrata (bloodfluke planorb)
 ORGANISM Biomphalaria glabrata
 Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora
 1 (bases 1 to 254)
 REFERENCE 1 (bases 1 to 254)
 AUTHORS Raghavan, N., Miller, A.N., Gardner, M., Fitzgerald, P.C., Kerlavage
 A.R., Johnston, D.A., Lewis, F.A. and Knight, M.
 TITLE Comparative gene analysis of Biomphalaria glabrata hemocytes pre-
 and post-exposure to miracidia of Schistosoma mansoni
 JOURNAL Mol. Biochem. Parasitol. 126 (2), 181-191 (2003)
 MEDLINE 22503446
 PUBMED 12615317
 COMMENT Contact: Raghavan N
 Biomedical Research Institute
 12111 Parklawn Dr., Rockville, MD 20852, USA
 Tel: 301-881-3300 ext.128
 Fax: 301-770-4756
 Email: nkrhelix.nih.gov, snailsrule@aol.com.
 FEATURES
 Source
 1. 254
 /organism="Biomphalaria glabrata"
 /mol_type="mRNA"
 /strain="BS-90"
 /db_xref="taxon:6526"
 /clone="RBGIG267R"
 /sex="hermaphrodite"
 /cell_type="hemocyte"
 /lab_host="Laboratory host"
 /clone_lib="Biomphalaria glabrata (BS-90)-unexposed lambda
 zap library"
 /note="Vector: pBluescript SK-. Site_1: EORI; Site_2:
 XhoI; Total RNA was isolated from the hemocytes of
 unexposed Biomphalaria glabrata (BS-90) snails and first
 strand cDNA synthesized using an oligo-dT primer-linker
 (XhoI). Second strand synthesis was followed by the
 ligation of EORI adaptors. Following digestion with XhoI,
 the completed, directional cDNA was cloned into Uni-ZAP
 XR phagemid vector by Stratagene.
 BASE COUNT 62 a 47 c 59 g 86 t
 ORIGIN
 Query Match 23.4%; Score 44; DB 9; Length 254;
 Best Local Similarity 61.1%; Pred. No. 13;
 Matches 88; Conservative 0; Mismatches 55; Indels 1; Gaps 1;
 Y 1 GTCGACGGTATCGATAGCTGATATCGAATTCGTGAT-CCGTTGCACATTTAAAGC 59
 |||||
 b 254 GTCGACGGTATCGATAGCTGATATCGAATTCGTGAT-CCGTTGCACATTTAAAGC 195
 Y 60 GGTGCAACTTTAAAGAGAGAAAGAGAGGTTGAAGAAAGGTTAGTAAAGTA 119
 |||||
 b 194 GAGTACATCCACATTAACAGCGGTATGAAAGTCAAGACGATTAATTACAGATATCA 135
 Y 120 TAAATACAGACCGGAGAGACTACGC 143
 |||||
 b 134 CAAGTAACGTCGCAACACACGCGC 111
 RESULT 5
 0791304/c 668 bp mRNA linear EST 12-FEB-2003
 DEFINITION BU791304 Schistosoma japonicum cDNA, mRNA sequence.
 ACCESSION BU791304
 VERSION BU791304.1 GI:28348311
 KEYWORDS EST
 SOURCE Schistosoma japonicum
 ORGANISM Schistosoma japonicum

TITLE Unpublished
 JOURNAL Expressed sequence tags from female adults of Schistosoma japonicum
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzgehc.sh.cn.
 FEATURES
 Source
 1. 668
 /organism="Schistosoma japonicum"
 /mol_type="mRNA"
 /db_xref="taxon:6182"
 /sex="female"
 /tissue_type="whole body"
 /dev_stage="adult"
 /lab_host="rabbits"
 /clone_lib="STP"
 BASE COUNT 184 a 112 c 101 g 271 t
 ORIGIN
 Query Match 23.1%; Score 43.4; DB 13; Length 668;
 Best Local Similarity 53.2%; Pred. No. 14;
 Matches 92; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
 Y 2 TCGACGGTATCGATAGCTGATATCGAATTCGTGATTCGTCAGCATTTAAAGCG 61
 |||||
 b 667 TCGACGGTATCGATAGCTGATATCGAATTCGTCAGCATTTAAAGCGATTCG 608
 Y 62 TTGCACTTTAAAGAGAGAAAGAGAGGTTGAAGAAAGGTTAGTAAAGTATA 121
 |||||
 b 607 GAAATTAATCTATTCCTCTGAAAGCAACGAAATCAATACGTTTATTTAAATCATTTA 548
 Y 122 AGTACAGACCGGAGAGATAGCCGCGCTGATTCGTTTAAAGAGAA 174
 |||||
 b 547 ACRATTCATTAACCAACAGCTGATGCTGATGATTAATTAACGATGAA 495
 RESULT 6
 B2571990 1017 bp DNA linear GSS 17-DEC-2002
 LOCUS msh2.2193.x1 msh Pseudomonas aeruginosa genomic clone msh2.2193,
 DEFINITION genomic survey sequence.
 ACCESSION B2571990
 VERSION B2571990.1 GI:27207051
 KEYWORDS GSS
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonas aeruginosa
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.
 REFERENCE 1 (bases 1 to 1017)
 AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
 Burns, J.L., Kaul, R. and Olsen, M.V.
 TITLE Whole-Genome-Sequence variation among multiple isolates of
 Pseudomonas aeruginosa library
 JOURNAL J. Bacteriol., (2002) In press
 COMMENT Contact: Chris K. Raymond
 Genome Center
 University of Washington
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066857244
 Email: craymond@u.washington.edu
 Class: Shotgun.
 FEATURES
 Location/Qualifiers

```

source
1. .1017
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="M5H"
/db_xref="taxon:287"
/clone="mah2_2193"
/clone_11b="msh"
/note="Environmental isolate. Whole genomic shotgun
library."
BASE COUNT      203 a      324 c      193 g      294 t      3 others
ORIGIN
Query Match      23.1%; Score 43.4; DB 29; Length 1017;
Best Local Similarity: 69.4%; Pred. No. 13;
Matches 59; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
OY 1 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTAAAGCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 55 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTAAAGCG 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTTGACAACTTTAAAGAGAGAGAA 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 GTTGAGAAAGTGGACGGGAGAA 139

RESULT 7
BU745817      1126 bp      mRNA      linear      EST 10-OCT-2002
LOCUS
DEFINITION
CH2#002_F0473 Canine heart normalized cDNA library in pBluescript
Canis familiaris cDNA clone CH2#002_F04 3', mRNA sequence.
ACCESSION
BU745817
VERSION
BU745817.1 GI:23695391
KEYWORDS
SOURCE
EST.
ORGANISM
Canis familiaris (dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 1126)
Y.Y., Desai, R., Olathe, M., Henthorn, P. and George A.L.
Expressed sequence tags from Canine heart
Unpublished
Other_FEATURES: CH2#002_F0477
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: a1.george@vanderbilt.edu
Insert Length: 2104 Std Error: 0.00
Seq primer: T3: ATTACCTCCTCCTAAAGGGA
High quality sequence start: 92
High quality sequence stop: 847.
Location/Qualifiers
1. .1126
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH2#002_F04"
/tissue="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)."
/clone_11b="Canine heart normalized cDNA library in
pBluescript"
/note="Organ: heart; Vector: pBluescript; Site: 1, 5' of
vector NotI; Site: 2, 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dt primed"
BASE COUNT      279 a      266 c      271 g      310 t
ORIGIN

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```

Query Match      23.1%; Score 43.4; DB 13; Length 1126;
Best Local Similarity: 66.7%; Pred. No. 13;
Matches 62; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
OY 1 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTAAAGCG 60.
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 57 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTAAAGCG 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTTGACAACTTTAAAGAGAGAGAAAGAGAGTT 93
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 117 GTTGAAACCTTCCACGTTTGATACAAAGAT 149

RESULT 8
CB169458
LOCUS
DEFINITION
RYE602702149.R1 CSEQFXL23 stomach-abomasum Bos taurus cDNA, mRNA
sequence.
ACCESSION
CB169458
VERSION
CB169458.1 GI:28155565
KEYWORDS
SOURCE
EST.
ORGANISM
Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 229)
Adelson, D.L. and Gill, C.A.
Bovine ESTs (Adelson and Gill)
Unpublished
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
1. .229
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue="stomach-abomasum"
/clone_11b="CSEQFXL23 stomach-abomasum"
/note="Organ: stomach-abomasum; Vector: pBluescript SK+;
Site: 1: NotI; Site: 2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNinsert)
GGGAATTGAGCTCCACCGCGGCGGCGCGCGCTCGAG. sequence 3' of
the inserts (AAGATTCGATTCAGAGCTTATGATACGCTGACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
BASE COUNT      61 a      52 c      59 g      57 t
ORIGIN
Query Match      23.0%; Score 43.2; DB 14; Length 229;
Best Local Similarity: 61.6%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
OY 1 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTAAAGCG 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 26 GTGACGGTATCGATTAAGCTTGATATGCAATTCGTCGATTCGTCGACGATTAAAGCG 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTTGACAACTTTAAAGAGAGAGAGAGAGAGTTAGTAA 112
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 AAGAGAAAGTGCATGAATTTGTTGAAGCTTAAAGGAGAGACTTAGAA 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
BZ561465
LOCUS
DEFINITION
pac2-164_3275.x4 pac2-164 Pseudomonas aeruginosa genomic clone
pac2-164_3275, genomic survey sequence.

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[illegible]

Db 210 ATTCGAATTACAAAGCA 193

RESULT 12
LOCUS B2556045 1098 bp DNA linear GSS 17-DEC-2002
DEFINITION pacsl-60_5483.x1 pacsl-60 Pseudomonas aeruginosa genomic clone
ACCESSION B2556045
VERSION B2556045.1 GI:27166248
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1098)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
source
1..1098
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone_lib="pacsl-60_5483"
/clone_1lb="pacsl-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."

BASE COUNT 218 a 325 c 360 g 195 t

ORIGIN

Query Match 22.8%; Score 42.8; DB 29; Length 1098;
Best Local Similarity 68.6%; Pred. No. 17;
Matches 59; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY 1 GTTCGACGGTATCGATATCGAATTCGTCGATCGGTGCACGATTAAAGCG 60
|||||
Db 64 GTTCGACGGTATCGAATTCGATATCGAATTCGTCGATCGGTGCACGAGGGCG 123
|||||
OY 61 GTTGACAACTTTAAAGAAAGAAA 86
|||||
Db 124 GGGGACACCATAGACCAAGCAAGCA 149
|||||

RESULT 13
LOCUS B2549869 708 bp DNA linear GSS 17-DEC-2002
DEFINITION pacsl-60_2384.x1 pacsl-60 Pseudomonas aeruginosa genomic clone
ACCESSION B2549869
VERSION B2549869.1 GI:27153450
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
REFERENCE Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 708)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol., (2002) In press

COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
source
1..708
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone_lib="pacsl-60_2384"
/clone_1lb="pacsl-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."

BASE COUNT 135 a 194 c 204 g 175 t

ORIGIN

Query Match 22.6%; Score 42.4; DB 29; Length 708;
Best Local Similarity 72.4%; Pred. No. 23;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 1 GTTCGACGGTATCGATATCGAATTCGTCGATCGGTGCACGATTAAAGCG 60
|||||
Db 52 GTTCGACGGTATCGAATTCGATATCGAATTCGTCGACGCCGTTCCCGCGCGCT 111
|||||
OY 61 GTTGACAACTTTAAAG 76
|||||
Db 112 CTTCACCTCTCTCAAA 127
|||||

RESULT 14
LOCUS B0744514 833 bp mRNA linear EST 10-OCT-2002
DEFINITION CH1#002.F10T3 Canine heart non-normalized cDNA library in
plasmid; Canis familiaris cDNA clone CH1#002.F10 3', mRNA
sequence.
B0744514
B0744514
ACCESSION B0744514.1 GI:23693350
VERSION B0744514
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 833)
Yi, Y., Desai, R., Olathe, M., Henthorn, P. and George A.L.
Expressed sequence tags from Canine heart
Unpublished
Other ESTs: CH1#002.F10T7
Contact: George A.L.
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert length: 1549 Std Error: 0.00
Seq primer: T3: ATTAACCTCTCACTAAGCA
High quality sequence start: 65
High quality sequence stop: 656.
Location/Qualifiers
1..833
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH1#002.F10"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)."

/clone.lib="Canine heart non-normalized cDNA Library in
pbluescript"
/note="Organ: heart; Vector: pbluescript; Site_1: 5' of
vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dr primed"

BASE COUNT 220 a 175 c 222 g 211 t 5 others

ORIGIN

Query Match 22.6%; Score 42.4; DB 13; Length 833;
Best Local Similarity 64.0%; Pred. No. 22;
Matches 64; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 GTGACGGATCGATAGCTGATATCGAATTCGTCGATTCGTCACGATTAAAGCG 60
|||||
DB 30 GTGACGGATCGATAGCTGATATCGAATTCCTTTTGGTTGTCAGTCCTGCTG 89
|||||
QY 61 GTTGACAACCTTTAAAGAGAAAGAAAGAGTTGAAGAA 100
|||||
DB 90 GTTTATTATTAAAGCAATTAATTTAGAAACAAATATA 129
|||||

RESULT 15
BU745422

LOCUS CH1#009_F03T3 Canine heart non-normalized cDNA Library in
DEFINITION pbluescript Canis familiaris cDNA clone CH1#009_F03 3', mRNA
sequence.

ACCESSION BU745422 958 bp mRNA linear EST 10-OCT-2002
VERSION BU745422
KEYWORDS BU745422.1 GI:23694771

SOURCE EST
ORGANISM Canis familiaris (dog)

Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 958)
AUTHORS Y.L.Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.

TITLE Expressed sequence tags from Canine heart

JOURNAL Unpublished

COMMENT Other_ESTs: CH1#009_F03T7

Contact: George AL
Division of Genetic Medicine

Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661

Email: al.george@vanderbilt.edu
Insert length: 1378 Std Error: 0.00

Seq primer: T3: ATTAACTCCTCACTTAAGGA
High quality sequence start: 90

High quality sequence stop: 759.

Location/Qualifiers

1..958
/organism="Canis familiaris"

/mol_type="mRNA"

/db_xref="taxon:9615"

/clone="CH1#009_F03"

/tissue_type="heart"

/cell_type="heart"

/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)"

/clone.lib="Canine heart non-normalized cDNA Library in
pbluescript"

/note="Organ: heart; Vector: pbluescript; Site_1: 5' of
vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dr primed"

BASE COUNT 310 a 208 c 166 g 274 t

ORIGIN

Query Match 22.6%; Score 42.4; DB 13; Length 958;
Best Local Similarity 60.3%; Pred. No. 22;
Matches 70; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GTGACGGATCGATAGCTGATATCGAATTCGTCGATTCGTCACGATTAAAGCG 60
|||||
DB 55 GTGACGGATCGATAGCTGATATCGAATTCCTTTTGGTTTAAAGAGATTAA 114
|||||

QY 61 GTTGACAACCTTTAAAGAGAAAGAAAGAGTTGAAGAAAGGCTAGTAAGTAA 116
|||||
DB 115 TTGACAAGTTTCACTTAGCGCAATACCTTAAGAAATTCGATACAGAGAA 170
|||||

Search completed: September 26, 2003, 10:15:44
Job time: 2204 secs